



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 192503**

**TO: Ruixiang Li**  
**Location: rem/4D75/4C70**  
**Art Unit: 1646**  
**Thursday, June 15, 2006**  
**Case Serial Number: 10/694438**

**From: Vira David**  
**Location: Biotech-Chem Library**  
**REM-1A41**  
**Phone: (571)272-1972**

**Virajita.David@uspto.gov**

### **Search Notes**

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Vira David  
Intern  
STIC Biotech/Chem Library  
(571)272-1110

78733

STIC-Biotech/ChemLib

192503

mg

From: Li, Ruixiang  
Sent: Saturday, June 10, 2006 8:43 AM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.10/694,438

Please do:

An oligomer search of SEQ ID NO: 2 against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2006, 12:17:23 ; Search time 17 Seconds  
(without alignments)  
528.040 Million cell updates/sec

Title: US-10-694-438-2  
Perfect score: 710  
Sequence: 1 MERTAGKELALPLQDWGE.....RDFMLRRKGRTNLVSFSS 710

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 64916 seqs, 12643201 residues

Word size : 1

Total number of hits satisfying chosen parameters: 64909

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB\_PEP.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB\_PEP.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB\_PEP.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB\_PEP.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB\_PEP.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB\_PEP.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB\_PEP.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	29.2	208	7	US-11-293-697-3953
2	8	1.1	133	6	US-10-953-349-20651
3	8	1.1	231	6	US-10-953-349-20650
4	8	1.1	265	6	US-10-953-349-20649
5	8	1.1	358	7	US-11-293-697-3662
6	8	1.1	575	6	US-10-953-349-6447
7	8	1.1	627	6	US-10-953-349-6446
8	8	1.1	642	6	US-10-505-928-259
9	8	1.1	664	6	US-10-953-349-6445
10	7	1.0	77	6	US-10-953-349-36948
11	7	1.0	78	6	US-10-953-349-36948
12	7	1.0	89	6	US-10-953-349-36483
13	7	1.0	91	6	US-10-953-349-39384
14	7	1.0	103	7	US-11-293-697-4841
15	7	1.0	111	6	US-10-953-393-3
16	7	1.0	119	6	US-10-953-349-30754
17	7	1.0	134	6	US-10-953-349-22783
18	7	1.0	138	6	US-10-953-349-39282
19	7	1.0	154	6	US-10-953-349-22782
20	7	1.0	154	6	US-10-953-349-25483
21	7	1.0	159	6	US-11-293-697-2997
22	7	1.0	167	6	US-10-953-349-22781
23	7	1.0	175	6	US-10-953-349-17915
24	7	1.0	183	6	US-10-953-349-5438
25	7	1.0	186	6	US-10-953-349-39281

ALIGNMENTS

RESULT 1

US-11-293-697-3953  
; Sequence 3953, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cdna  
; FILE REFERENCE: HI-A0106  
; CURRENT APPLICATION NUMBER: US/11/293.697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108.260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3953  
; LENGTH: 208  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3953

Query Match 29.2%; Score 207; DB 7; Length 208;  
Best Local Similarity 100.0%; Pred. No. 78-186;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	237	MPQGPQLLDFSVDEVAEQTLIDLELFSKVLVECLGSVMSQDRPCGAAGASPTVRATVA	296
Db	1	MPQGPQLLDFSVDEVAEQTLIDLELFSKVLVECLGSVMSQDRPCGAAGASPTVRATVA	60
Qy	297	QFNTVTGCVLGSVLGAPLAAPQRAQRLKWIIRIAQRCRELRFSSRLAISALQSNPIY	356
Db	61	QFNTVTGCVLGSVLGAPLAAPQRAQRLKWIIRIAQRCRELRFSSRLAISALQSNPIY	120
Qy	357	RLKRSWGVSRPLSTFRKLSQIFSDNNHLSREILFQEEATGSGQEEEDNTPGSLSPKP	416
Db	121	RLKRSWGVSRPLSTFRKLSQIFSDNNHLSREILFQEEATGSGQEEEDNTPGSLSPKP	180
Qy	417	PPGFPVPLGFTFLDVLMDLTDALPDMLE	443
Db	181	PPGFPVPLGFTFLDVLMDLTDALPDMLE	207

RESULT 2

US-10-953-349-20651  
; Sequence 20651, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

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Db      251 SQIFSDEN 258
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RESULT 5
US-11-293-697-3662
; Sequence 3662, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELEX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3662
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3662
Query Match      1.1%; Score 8; DB 7; Length 358;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      550 SVSPGSGPP 557
      |||||
Db      288 SVSPGSGPP 295

RESULT 6
US-10-953-349-6447
; Sequence 6447, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6447
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6447
Query Match      1.1%; Score 8; DB 6; Length 575;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      544 PSSPTSSV 551
      |||||
Db      485 PSSPTSSV 492

RESULT 7
US-10-953-349-6446
; Sequence 6446, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252

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; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6446  
; LENGTH: 627  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-6446

Query Match 1.1%; Score 8; DB 6; Length 627;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 PSSPTSSV 551  
|||||  
Db 537 PSSPTSSV 544

RESULT 8  
US-10-505-928-259  
; Sequence 259, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 259  
; LENGTH: 642  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-259

Query Match 1.1%; Score 8; DB 6; Length 642;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 WGEETEDG 24  
|||||  
Db 211 WGEETEDG 218

RESULT 9  
US-10-953-349-6445  
; Sequence 6445, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6445  
; LENGTH: 664  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-6445

Query Match 1.1%; Score 8; DB 6; Length 664;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 PSSPTSSV 551  
|||||  
Db 574 PSSPTSSV 581

RESULT 10  
US-10-953-349-36948  
; Sequence 36948, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 36948  
; LENGTH: 77  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-36948

Query Match 1.0%; Score 7; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 552 SPGSPPS 558  
|||||  
Db 56 SPGSPPS 62

RESULT 11  
US-10-953-349-36484  
; Sequence 36484, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 36484  
; LENGTH: 78  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-36484

Query Match 1.0%; Score 7; DB 6; Length 78;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 SSSPPSGS 540  
|||||  
Db 15 SSSPPSGS 21

RESULT 12  
US-10-953-349-36483  
; Sequence 36483, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 36483  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-36483

US-10-953-349-36483

Query Match 1.0%; Score 7; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 SSSPSGS 540  
Db 26 SSSPSGS 32  
|||||

## RESULT 13

US-10-953-349-29384  
; Sequence 29384, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 29384  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-953-349-29384

Query Match 1.0%; Score 7; DB 6; Length 91;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 PSSPTSS 550  
Db 46 PSSPTSS 52  
|||||

## RESULT 14

US-11-293-697-4841  
; Sequence 4841, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; FILE REFERENCE: H1-A0106  
; TITLE OF INVENTION: Novel full length cDNA  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4841  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-4841

Query Match 1.0%; Score 7; DB 7; Length 103;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 DRPGAAG 286  
Db 46 DRPGAAG 52  
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## RESULT 15

US-10-953-393-3  
; Sequence 3, Application US/10953393  
; Publication No. US2006008851A1  
; GENERAL INFORMATION:

; APPLICANT: Ayyavoo, Velpandi  
; APPLICANT: Patel, Mamata  
; APPLICANT: Kieber-Emmons, Thomas  
; APPLICANT: Weiner, David B.  
; APPLICANT: Mahalingam, Sundaramy  
; TITLE OF INVENTION: Functional Fragments of HIV-1 VPR Protein and Methods  
; FILE REFERENCE: UPN-4023  
; CURRENT APPLICATION NUMBER: US/10/953,393  
; CURRENT FILING DATE: 2004-09-29  
; PRIOR APPLICATION NUMBER: US/09/485,421  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/055,754  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence  
US-10-953-393-3

Query Match 1.0%; Score 7; DB 6; Length 111;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 PPPPPG 124  
Db 104 PPPPPG 110  
|||||

Search completed: June 12, 2006, 12:20:40  
Job time : 17 secs

November 2005

Published\_Applications\_Nucleic\_Acid\_and\_Published\_Applications\_Amino\_Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic\_Acid\_Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New). Searches run against Amino\_Acid\_Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC search.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 12, 2006, 11:56:13 ; Search time 304 Seconds  
(without alignments)

2160.398 Million cell updates/sec

Title: US-10-694-438-2

Perfect score: 710  
Sequence: 1 MERTAGKELALAPLQDWGEE.....RDFMLRRKRGTRNTLSVSPS 710

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: UniProt\_7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609	85.8	710	2 Q3MIN7_HUMAN	Q3min7 homo sapien
2	402	56.6	497	2 Q8TEP0_HUMAN	Q8tepo homo sapien
3	447	6.6	505	2 Q9DBL8_MOUSE	Q9dbls mus musculu
4	47	6.6	505	2 Q6KAR7_MOUSE	Q6kar7 mus musculu
5	47	6.6	687	2 Q8BKX3_MOUSE	Q8bkx3 mus musculu
6	47	6.6	709	2 Q3UY15_MOUSE	Q3uy15 mus musculu
7	47	6.6	709	2 Q924M8_MOUSE	Q924m8 mus musculu
8	47	6.6	709	2 Q9JID4_MOUSE	Q9jid4 mus musculu
9	17	2.4	309	2 Q5T7U6_HUMAN	Q5t7u6 homo sapien
10	17	2.4	411	2 Q8N4Y1_HUMAN	Q8n4y1 homo sapien
11	17	2.4	555	2 Q3UEA9_MOUSE	Q3uea9 mus musculu
12	17	2.4	625	2 Q8NFE1_HUMAN	Q8nfe1 homo sapien
13	17	2.4	745	2 Q9P2N8_HUMAN	Q9p2n8 homo sapien
14	17	2.4	824	2 Q8TEK9_HUMAN	Q8tek9 homo sapien
15	17	2.4	840	2 Q3UY09_MOUSE	Q3uy09 mus musculu
16	17	2.4	852	2 GNDS_MOUSE	Q033b8 mus musculu
17	17	2.4	852	2 Q8R0T7_MOUSE	Q8r0t7 mus musculu
18	17	2.4	859	2 Q6KX11_HUMAN	Q6kx11 homo sapien
19	17	2.4	895	1 GNDS_RAT	Q033b6 rattus norv
20	17	2.4	895	2 Q3TXZ3_MOUSE	Q3txz3 mus musculu
21	17	2.4	902	2 Q6PCF1_HUMAN	Q6pcf1 homo sapien
22	17	2.4	907	2 Q3TWC1_MOUSE	Q3twc1 mus musculu
23	17	2.4	913	2 Q6ZSD5_HUMAN	Q6zsd5 homo sapien
24	17	2.4	914	1 GNDS_HUMAN	Q12967 homo sapien
25	17	2.4	924	2 Q5T7V4_HUMAN	Q5t7v4 homo sapien
26	17	2.4	924	2 Q6ZPU1_MOUSE	Q6zpu1 mus musculu
27	15	2.1	782	2 Q4S7S0_TETNG	Q4s7s0 tetradon n
28	13	1.8	933	2 Q4RPV7_TETNG	Q4rpv7 tetradon n
29	12	1.7	804	2 Q6P112_BRARE	Q6p112 brachydanio
30	11	1.5	78	2 Q57412_TETFL	Q57412 tetradon f
31	11	1.5	359	2 Q9DE48_BRARE	Q9de48 brachydanio

32	11	1.5	742	2 Q4SD50_TETNG	Q4sd50 tetradon n
33	11	1.5	766	2 Q5RDR4_PONPY	Q5rd4 pongo pygma
34	11	1.5	768	1 RGL1_HUMAN	Q9z16 homo sapien
35	11	1.5	768	1 RGL1_MOUSE	Q60695 mus musculu
36	11	1.5	768	2 Q5VU93_HUMAN	Q5vu93 homo sapien
37	11	1.5	768	2 Q8VD09_MOUSE	Q8vd09 m rat guani
38	11	1.5	768	2 Q5Z1Y0_CHICK	Q5z1y0 gallus gall
39	11	1.5	803	2 Q5VU94_HUMAN	Q5vu94 homo sapien
40	11	1.5	803	2 Q7Z3U6_HUMAN	Q7z3u6 homo sapien
41	10	1.4	372	2 Q5C1L6_SCHJA	Q5c1l6 schistosoma
42	10	1.4	765	2 Q5TR60_ANOGA	Q5tr60 anopheles g
43	10	1.4	774	2 Q86B12_DROME	Q86b12 drosophila
44	10	1.4	774	2 Q9GR11_DROME	Q9gr11 drosophila
45	10	1.4	860	2 Q19852_CAEEL	Q19852 caenorhabdi

## ALIGNMENTS

RESULT 1  
Q3MIN7\_HUMAN PRELIMINARY; PRT; 710 AA.  
AC Q3MIN7;  
DT 25-OCT-2005, integrated into UniProtKB/TREMBL.  
DT 25-OCT-2005, sequence version 1.  
DT 21-FEB-2006, entry version 5.  
DE Rat guanine nucleotide dissociation stimulator-like 3.  
GN Name=RGL1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung and heart;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
RA Datchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uding T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huijx S.W.,  
RA Vallalun D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
PL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung and heart;  
RG NIH MGC Project;  
RL Submitted (Aug-2005) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung and heart;  
RG NIH MGC Project;  
RL Submitted (Jan-2006) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; BC101756; AA101757.1; -; mRNA.  
DR EMBL; BC11958; AA11959.1; -; mRNA.

ID	AC	SEQUENCE	Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps
ID	AC	SEQUENCE	Matches	709;	Conservative	0;	Mismatches	1;	Indels	0;
DR	GO	GO:0005085; F-guanyl-nucleotide exchange factor activity; IEA.								
DR	GO	GO:0007264; P-small GTPase mediated signal transduction; IEA.								
DR	InterPro	IPR000159; RA.								
DR	InterPro	IPR000651; Rasgef_N.								
DR	InterPro	IPR001895; RasGRF_CDC25.								
DR	Pfam	PF00788; RA; 1.								
DR	Pfam	PF00617; RasGEF; 1.								
DR	SMART	SM00314; RA; 1.								
DR	SMART	SM00147; RasGEF; 1.								
DR	SMART	SM00229; RasGEFN; 1.								
DR	PROSITE	PS00200; RA; 1.								
DR	PROSITE	PS00720; RasGEF; 1.								
DR	PROSITE	PS00009; RasGEF_CAT; 1.								
DR	PROSITE	PS00212; RasGEF_NTER; 1.								
DR	SEQUENCE	710 AA; 78107 MW; E36F9B3C543E6757 CRC64;								
QY		1 MERTAGKEIALALPIODMGEETEDGAVSYSLRORSQRSPAEQGGSGAPSPINATFLH	85.8%;	Score 609;	DB 2;	Length 710;				
Db		1 MERTAGKEIALALPIODMGEETEDGAVSYSLRORSQRSPAEQGGSGAPSPINATFLH	99.9%;	Pred. No. 0;	Mismatches 1;	Indels 0;	Gaps 0;			
QY		61 YRTSKVRVLRARLERLVGELVFGREODPSMPAPFLATYRTFVPACILGFLPMPPP								
Db		61 YRTSKVRVLRARLERLVGELVFGREODPSMPAPFLATYRTFVPACILGFLPMPPP								
QY		121 PPGGEIKKTAVQDLSFNNLRAVSVYGSWLODHPDRDHPVSDIGSVTFPGMAP								
Db		121 PPGGEIKKTAVQDLSFNNLRAVSVYGSWLODHPDRDHPVSDIGSVTFPGMAP								
QY		181 GSAEAKAKLELDEPLEAEAREQEEBPQVMTGPPRVAQTSDPDSEACAEKEEGIMEQG								
Db		181 GSAEAKAKLELDEPLEAEAREQEEBPQVMTGPPRVAQTSDPDSEACAEKEEGIMEQG								
QY		241 POLDPSFDEVAEQTLTLDLEFSKRYLYECGYSWSQDRPGGAAGAPTYVATTAQENT								
Db		241 POLDPSFDEVAEQTLTLDLEFSKRYLYECGYSWSQDRPGGAAGAPTYVATTAQENT								
QY		301 VTGCVLGSVLGAPGLAPOPRAORLEKRIIRAORCELRNFSSLRALISALQSNPTYRLKR								
Db		301 VTGCVLGSVLGAPGLAPOPRAORLEKRIIRAORCELRNFSSLRALISALQSNPTYRLKR								
QY		361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATIEGQSEEDNTPGSLPSKPPGP								
Db		361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATIEGQSEEDNTPGSLPSKPPGP								
QY		421 VPIYGTFLTDLVMTLALPDMLEGLINFEKRRKWEILARIQOLQRCCOSYTLSPHPPI								
Db		421 VPIYGTFLTDLVMTLALPDMLEGLINFEKRRKWEILARIQOLQRCCOSYTLSPHPPI								
QY		481 LAALHAQNLTEEQSYRLSRVIEPPAASCPSRPRIIRRLISLTKRLSAKLAEKSSPSGS								
Db		481 LAALHAQNLTEEQSYRLSRVIEPPAASCPSRPRIIRRLISLTKRLSAKLAEKSSPSGS								
QY		541 PGDPSPTSSVSPGSPSPSRDPAASPPSPQSPSTKLPLSLDPSRPPLPLG								
Db		541 PGDPSPTSSVSPGSPSPSRDPAASPPSPQSPSTKLPLSLDPSRPPLPLG								
QY		601 SPRIPPLPAQGSSEARVIRVSDINDHGNLYRSILLTNSQKAPSVVRALQKHNVPQMACD								
Db		601 SPRIPPLPAQGSSEARVIRVSDINDHGNLYRSILLTNSQKAPSVVRALQKHNVPQMACD								
QY		661 YQLQVQLPGRVLLIPDNANFYAMSPLVAPRDPFMLRKEGRNTLSVSPS								
Db		661 YQLQVQLPGRVLLIPDNANFYAMSPLVAPRDPFMLRKEGRNTLSVSPS								

DT	01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT	01-JUN-2002, sequence version 1.
DT	07-FEB-2006, entry version 15.
DE	FLJ00153 protein (Fragment).
GN	Name=FLJ00153;
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC	Homo.
OX	NCBI_TaxID=9606;
RN	(1)
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Spleen;
RA	Jikuya H., Takano J., Nomura N., Kixuno R., Nagase T., Ohara O.;
RL	Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC	-----
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	-----
DR	EMBL; AK074082; BAB84908.1; -; mRNA.
DR	HSSP; Q03386; 1LFD.
DR	Ensembl; ENSG00000187266; Homo sapiens.
DR	GO; GO:0005085; P:guanylyl-nucleotide exchange factor activity; IEA.
DR	GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR	InterPro; IPR001591; RA.
DR	InterPro; IPR001895; RasGRF_CDC25.
DR	Pfam; PF00788; RA; 1.
DR	Pfam; PF00617; RasGEF; 1.
DR	SMART; SMO0147; RasGEF; 1.
DR	PROSITE; PS00720; RasGEF; 1.
DR	PROSITE; PS50009; RasGEF_CAT; 1.
FT	NON TER 1 1
SQ	SEQUENCE 497 AA; 54312 MW; F78318B92826F537 CRC64;
 Query Match 56.6%; Score 402; DB 2; Length 497;	
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	213 GPPEVAQTSPDPSSEACAEEEEGIMPGQPQLDFSVDEVAAEOLTLIDLELFISKVLYECL 272
Db	10 GPPVAQTSPDPSSEACAEEEGIMPGQPQLDPSVDEVAEQTLIDLELFISKVLYECL 69
QY	273 GSWSQDPDRPCAGASPTVRATVAQENTVTTCVIGSYLGAPGLAAPORAOELEKIRIAQ 332
Db	70 GSWSQCDRGCAGASPTVRATVAQENTVTTCVIGSYLGAPGLAAPORAOELEKIRIAQ 129
QY	333 RCRELNRFPSSLRIALSLAQSNPIYTRLRSMGAVSREPLSTFRKLSQLFSDENNHLSREI 392
Db	130 RCRELNRFPSSLRIALSLAQSNPIYTRLRSMGAVSREPLSTFRKLSQLFSDENNHLSREI 189
QY	393 LFOEATEGSQEEDNTFGSLPSKPPEGVPVYLGTFLTDLVMDLTALPDMLGGDLINFEKR 452
Db	190 LFQEAETSGSQEENPTGSLPSKPPGPVPVYLGTFLTDLVMDLTALPDMLGGDLINFEKR 249
QY	453 RKKEELIARIQOIORCQSITLSPHPILTAHAONOLTEQSRUSRVIEPPAACSPSS 512
Db	250 RKKEELIARIQOIORCQSITLSPHPILTAHAONOLTEQSRUSRVIEPPAACSPSS 309
QY	513 PRIARRISLTKRLSAKLAREKSSPSGSDPDSPTSVSVPGPSPPSSPRGRDA PAGSPA 572
Db	310 PRIARRISLTKRLSAKLAREKSSPSGSDPDSPTSVSVPGPSPPSSPRGRDA PAGSPA 369
QY	573 SPQGQGSTKLPLSLDSPRRPALPLGSGRIRLLPAQQSSEA 614
Db	370 SPQGQGSTKLPLSLDSPRRPALPLGSGRIRLLPAQQSSEA 411
 RESULT 3	
Q9DBLA_MOUSE PRELIMINARY; PRT; 343 AA.	
Q9DBLB_MOUSE INTEGRATED INTO UNIPROTKB/TRMBL.	
Q9DBLB; 01-JUN-2001, integrated into UniProtKB/TrEMBL.	



RT RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer."  
 RL Genome Res. 10:1757-1771(2000).  
 RN [8].  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RA Aachai J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
 RA Imotani K., Ishii Y., Iton H., Iwata M., Kasukawa T., Kato H.,  
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
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DR EMBL: AK004876; BAB23634.1; -; mRNA.  
 DR MGI: MGI:1918996; Rg13.  
 DR GO: GO:0005515; F:Protein binding; IPI.  
 DR GO: GO:0008321; F:Rat guanylyl-nucleotide exchange factor activity; IDA.  
 DR GO: GO:0017016; F:Ras GTPase binding; IDA.  
 DR GO: GO:0007218; F:neuropeptide signaling pathway; RCA.  
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; TAS.  
 DR InterPro: IPR001895; RasGRF\_CDC25.  
 DR Pfam: PF00617; RasGRF\_1.  
 DR SMART: SM00147; RasGRF\_1.  
 DR PROSITE: PS50009; RASGEF\_CAT; 1.  
 DR SEQUENCE 343 AA; 37517 MW; B66A576AE9B973A9 CRC64;  
 SQ

Query Match 6.6%; Score 47; DB 2; Length 343;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-35;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 325 EKWIRIARCRRLRNPSLRATLSALQSNPIYRLKRSWGAVSRPPLS 371  
 DB 227 EKWIRIARCRRLRNPSLRATLSALQSNPIYRLKRSWGAVSRPPLS 273

RESULT 4  
 ID Q6KAR7\_MOUSE PRELIMINARY; PRT; 505 AA.  
 AC Q6KAR7;  
 DT 05-JUL-2004; integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004; sequence version 1.  
 DT 07-FEB-2006; entry version 11.  
 DE MFL000153 protein (Fragment).  
 GN Name=Rg13; Synonyms=MFLJ00153;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN [1].  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=embryonic tail;  
 RA Okazaki N., Kikuno R., Ohara R., Imamoto S., Koseki H., Hiraoka S.,  
 RA Suga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.,  
 RA "Prediction of the Coding Sequences of Mouse Homologues of FLY Genes:  
 RT The Complete Nucleotide Sequences of 110 Mouse FLY-Homologous cDNAs  
 RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly  
 RT Sampled from Size-Fractionated Libraries";  
 RL DNA Res. 11:167-180(2004).  
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DR EMBL: AK131140; BAD21390.1; -; -;  
 DR MGI: MGI:1918996; Rg13.  
 DR GO: GO:0005515; F:Protein binding; IPI.  
 DR GO: GO:0008321; F:Rat guanylyl-nucleotide exchange factor activity; IDA.  
 DR GO: GO:0017016; F:Ras GTPase binding; IDA.  
 DR GO: GO:0007218; F:neuropeptide signaling pathway; RCA.  
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; TAS.  
 DR InterPro: IPR001895; RasGRF\_CDC25.  
 DR InterPro: IPR001895; RasGRF\_CDC25.  
 DR Pfam: PF00788; RA; 1.  
 DR Pfam: PF00617; RasGRF\_1.  
 DR SMART: SM00147; RasGRF\_1.  
 DR PROSITE: PS50200; RA; 1.  
 DR PROSITE: PS00720; RASGEF\_1.  
 DR PROSITE: PS50009; RASGEF\_CAT; 1.  
 FT NON TER 1 1  
 FT NON TER 505 505  
 SQ SEQUENCE 505 AA; 55486 MW; 85333D2A74ED0CA1 CRC64;  
 SQ

Query Match 6.6%; Score 47; DB 2; Length 505;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-35;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 325 EKWIRIARCRRLRNPSLRATLSALQSNPIYRLKRSWGAVSRPPLS 371  
 DB 147 EKWIRIARCRRLRNPSLRATLSALQSNPIYRLKRSWGAVSRPPLS 193

RESULT 5  
 ID Q6KRD3\_MOUSE PRELIMINARY; PRT; 687 AA.  
 AC Q6KRD3;  
 DT 01-MAR-2003; integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003; sequence version 1.  
 DT 07-FEB-2006; entry version 20.  
 DE 0 day neonate eyeball cDNA. RIKEN full-length enriched library,  
 DE clone:EI30107B16 product:RALGDS-RELATED EFFECTOR PROTEIN OF M-RAS,  
 DE full insert sequence.  
 GN Name=Rg13;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN [1].  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=eyeball;  
 RC PubMed:16141072; DOI:10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA Di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
 RA Flechter C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 RA Gusella J.S., Harbers M., Hayashizaki Y., Hensch T.K., Hirokawa N.,  
 RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Ijima A., Ishikawa T.,  
 RA Jaki M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,

RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Noji F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavasi G., Pesole G.,  
 RA Petrovsky N., Plaza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Roit B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
 RA Schonbach C., Seliguchi K., Semple C.A., Sento S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sincclair B.,  
 RA Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K.,  
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yaig K.,  
 RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Yamanouchi S.M., Zaslavsky R.D., Liu E.T., Brusic V., Quackenbush J.,  
 RA Wallestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 RA Kawauchi T., Kojima M., Kondo S., Kono H., Nakano K., Nimomiya N.,  
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watanishi A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.";   
 RL Science 309:1559-1563 (2005).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 RC (Genome Network Core Team) and the PANTOM Consortium;  
 RT "Antisense transcription in the mammalian transcriptome.";   
 RL Science 309:1564-1566 (2005).  
 [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;  
 RX PubMed=22354683; PubMed=14466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osaeto N., Saito R., Suzuki H., Yamashita I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirini L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Drgani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Guelinich S., Hayakawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., Kling B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lehar B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mili H.,  
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 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
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 RA Sandelin A., Schneider C., Semple C.A., Secou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wallestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang J., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shigaoka A.,  
 RA Yamashita A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";   
 RL Nature 420:563-573 (2002).  
 [5]  
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 RC STRAIN=C57BL/6J; TISSUE=Eyeball;  
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 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
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RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schirini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Baren G.,  
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 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
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 RL Nature 409:685-690 (2001).  
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 RT "Normalization and subcloning of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";   
 RL Genome Res. 10:1617-1630 (2000).  
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 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";   
 RL Genome Res. 10:1757-1771 (2000).  
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 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T.,  
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 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
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 CC Distributed under the Creative Commons Attribution-NonDerivs license  
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 DT 07-FEB-2006, entry version 5.  
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RA Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
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 RA Tagami M., Waki K., Watanishi A., Okamura-Oho Y., Suzuki H., Kawai J.,  
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 RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
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 RC PubMed=16141073; DOI=10.1126/science.1112009;  
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 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
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 RT "Antisense transcription in the mammalian transcriptome.";  
 RL Science 309:1564-1566(2005).  
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 RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
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 RL Nature 420:563-573(2002).  
 RN [5]  
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 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;  
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 RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690 (2001).  
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RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).  
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RA Okaaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
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RA Shibata K., Shitaki T., Tagami M., Tagami Y., Waki K., Watabiki A.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
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DR GO:GO:0007218; F:neuropeptide signaling pathway; RCA.  
DR GO:GO:0007264; P:small GTPase mediated signal transduction; TAS.  
DR GO:GO:0007264; P:small GTPase mediated signal transduction; TAS.  
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DR InterPro:IPR000651; RasGEF.N.  
DR InterPro:IPR018953; RasGRF\_CDC25.  
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DR SMART:SM00229; RasGEFN.1.  
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RX MEDLINE:21214408; PubMed:11313946; DOI=10.1038/sj.onc.1204053;
RA Ehrhart G.R., Korthier C., Wieler J.S., Knaus M., Schrader J.W.;
RT "A novel potential effector of M-Ras and p21 Ras negatively regulates
RT p21 Ras-mediated gene induction and cell growth.";
RN Oncogene 20:188-197(2001).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RA Ehrhart G.R.A., Schrader J.W.;
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
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DR EMBL, AF239661; AAK9126.1; -; mRNA.
DR HSSP, Q61193; 1RLF.
DR Ensemble, ENSMUSG00000040146; Mus musculus.
DR MGI, MGI:1918996; Rgl3.
DR GO, GO:0005515; P:protein binding; IPI.
DR GO, GO:0008321; F:Rat guanyl-nucleotide exchange factor activity; IDA.
DR GO, GO:0017016; F:Ras GTPase binding; IDA.
DR GO, GO:0007218; P:neuropeptide signaling pathway; RCA.
DR GO, GO:0007264; P:small GTPase mediated signal transduction; RCA.
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DR PROSITE, PS50212; RasGEF_NTER; 1.
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Query Match 6.6%; Score 47; DB 2; Length 709;
Best Local Similarity 100.0%; Pred. No. 2,3e-35;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 325 EKWIRIAQRCCELNFSSLRALISALQSNPIYLKRSWGAVSREPLS 371
Db 326 EKWIRIAQRCCELNFSSLRALISALQSNPIYLKRSWGAVSREPLS 372

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DT 07-FEB-2006, entry version 19.
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RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20418060; PubMed=10869344;
RA Shao H., Andres D.A.;
RT "A novel RasGEF-like protein, RGH3, as a candidate effector for rit
and Ras".
RL J. Biol. Chem. 275:26914-26924(2000).
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DR GO; GO:0008321; F:Rai guanyl-nucleotide exchange factor activity; IDA.
DR GO; GO:0017016; F:Ras GTPase binding; IDA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; RCA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; RCA.
DR InterPro; IPR000159; RasGEF_N.
DR InterPro; IPR001895; RasGEF_N.
DR Pfam; PF00788; RA; 1.
DR Pfam; PF00617; RasGEF; 1.
DR Pfam; PF00618; RasGEF_N; 1.
DR SMART; SM00314; RA; 1.
DR SMART; SM00147; RasGEF; 1.
DR SMART; SM00229; RasGEFN; 1.
DR PROSITE; PS50200; RA; 1.
DR PROSITE; PS00720; RasGEF; 1.
DR PROSITE; PS50009; RasGEF_CAT; 1.
DR PROSITE; PS50212; RasGEF_NTER; 1.
SQ SEQUENCE 709 AA; 77973 MW; 60F7CAF8138AB609 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 709;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 325 EKWIRIACRCRELNFSLSLRAISALQSNPIYRLKRSMAVSEPLS 371
DB 326 EKKIRIAQRCRELNFSLSLRAISALQSNPIYRLKRSMAVSEPLS 372

RESULT 9
QSTU6_HUMAN
ID QSTU6_HUMAN PRELIMINARY; PRT; 309 AA.
AC QSTU6;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Rai guanine nucleotide diisocytide stimulator (Fragment).
GN Name=RALGDS; ORFNames=RP11-326L24.1-010;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RA Kimberley A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; AL162417; CA113414.1; -, Genomic DNA.
DR Ensembl; ENSG00000160271; Homo sapiens.
DR GO; GO:0005085; P:guanyl-nucleotide exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR001895; RasGEF_CDC25.
DR Pfam; PF00617; RasGEF; 1.

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DR SMART; SM00147; RasGEF; 1.
DR PROSITE; PS00720; RasGEF; 1.
DR PROSITE; PS50009; RasGEF_CAT; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 309 AA; 34707 MW; 41CFPF7A9DA84A9B CRC64;

Query Match
Best Local Similarity 100.0%; Score 17; DB 2; Length 309;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 VPYLGFTLTDVLMDDTA 437
DB 124 VPYLGFTLTDVLMDDTA 140

RESULT 10
Q8N4Y1_HUMAN
ID Q8N4Y1_HUMAN PRELIMINARY; PRT; 411 AA.
AC Q8N4Y1;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC033198; AAH33198.1; -, mRNA.
DR HSSP; Q12967; 2RCF.
DR SMR; Q8N4Y1; 294-380.
DR Ensembl; ENSG00000160271; Homo sapiens.
DR GO; GO:0005085; P:guanyl-nucleotide exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR000159; RA.
DR InterPro; IPR001895; RasGEF_CDC25.
DR Pfam; PF00788; RA; 1.
DR Pfam; PF00617; RasGEF; 1.
DR SMART; SM00314; RA; 1.
DR PROSITE; PS50200; RA; 1.
DR PROSITE; PS00720; RasGEF; 1.
DR PROSITE; PS50009; RasGEF_CAT; 1.
FT Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 411 AA; 45526 MW; 114CF1F26F92B79 CRC64;

Query Match
Best Local Similarity 100.0%; Score 17; DB 2; Length 411;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 VPYLGFTLTDVLMDDTA 437
DB 61 VPYLGFTLTDVLMDDTA 77

RESULT 11
Q3UEA9_MOUSE
ID Q3UEA9_MOUSE PRELIMINARY; PRT; 555 AA.
AC Q3UEA9;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Bone marrow macrophage cDNA, RIKEN full-length enriched library,

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DE clone:G530007E09 product:rat guanine nucleotide dissociation  
stimulator, full insert sequence. (Fragment).  
CN Name:RatGds.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
NCBI\_Taxid:10090;  
OC [1]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methode Enzymol. 303:19-44(1999).  
[2]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
Davis M.J., Wilmink L.G., Aidinis V., Allen J.E.,  
Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
Banaal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
Crocce M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
Fleischer C.F., Fukushima T., Furuno M., Fukui S., Gariboldi M.,  
Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,  
Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
Liu S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
Mottacqui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,  
Nilsen R., Nishiguchi S., Nishikawa S., Noi F., Ohtsuka O.,  
Okazaki Y., Oriando V., Pang K.C., Pavan W.T., Pavoni G., Pesole G.,  
Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
Schonbach C., Sekiguchi K., Semple C.A., Sessa L., Sheng Y.,  
Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
Sperling S., Stupka E., Sugtara K., Sultana R., Takenawa Y., Taki K.,  
Tamura K., Tan S.L., Tang S., Taylor W.S., Tegler J., Teichmann S.A.,  
Ueda H.R., van Nimwegen E., Verardo R., Wei C., Yang J., Yang K.,  
Yamanishi H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C.,  
Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Nimura N.,  
Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
Tagami M., Waki K., Watanabe A., Okamura-Ohno Y., Suzuki H., Kawai J.,  
Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";  
RL Science 309:1559-1563(2005).  
[3]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group, and Genome Science Group  
(Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).  
[4]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX MEDLINE=22354683; PubMed=12465851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
Nikaido I., Otsu N., Saito R., Suzuki H., Yamashita I., Kiyosawa H.,  
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
BALDARELLI R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
Schrini L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
Blake J.A., Brad D., Brusic V., Chothia C., Cobani L.E., Cousins S.,  
Dalla E., Dragani T.A., Fletcher C.F., Forrest A.R., Fraser K.S.,  
GAsterland T., Gariboldi M., Gissi C., Gockik A., Gough J.,  
R. GRIMMOND S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
Kana A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
Maggioli D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G.,  
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
Sandelin A., Schneider C., Semple C.A., Setou R., Shimada K.,  
Sultana R., Takenawa Y., Taylor M.S., Teasdale R.D., Tomita K.,  
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
Wilmink L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,  
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[5]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamashita I.,  
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,  
Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,  
Schrini L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,  
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,  
Nordine P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,  
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,  
Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[6]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,  
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[7]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kikunishi T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
Fujiwara S., Inoue K., Togawa K., Izawa M., Ohara Y., Watanabe K.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).

[8]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
RA Hori F., Iida J., Imamura K., Imciani K., Itoh M., Kanagawa S.,  
RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Nishimura N.,  
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,  
RA Muramatsu M., Hayashizaki Y.,  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
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CC -----  
CC EMBL: AK149644; BAE2902.1; -; mRNA.  
DR MGI: MGI:107485; Ralgsds.  
DR GO: GO:0008289; F:lipid binding; RCA.  
DR GO: GO:0005515; F:protein binding; IPI.  
DR GO: GO:0006810; P:transport; RCA.  
DR InterPro: IPR001895; RasGRF\_CDC25.  
DR Pfam: PF00788; RA; 1.  
DR SMART: SM00617; RasGEF; 1.  
DR SMART: SM00147; RasGEF; 1.  
DR PROSITE: PS50200; RA; 1.  
DR PROSITE: PS00720; RasGEF; 1.  
DR PROSITE: PS50009; RasGEF\_CAT; 1.  
FT NON TER 1 1  
SQ SEQUENCE 555 AA; 62049 MW; 8F2ACB72F59BD04B CRC64;  
  
Query Match 2.4%; Score 17; DB 2; Length 555;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 421 VPIYGTFLTDLVMLDPTA 437  
Db 205 VPIYGTFLTDLVMLDPTA 221  
  
RESULT 12  
O8NFP31\_HUMAN PRELIMINARY; PRT; 625 AA.  
AC O8NFP31;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 12.  
DE FLJ00371 protein (Fragment).  
GN Name=FLJ00371;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
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CC -----  
CC EMBL: AK090450; BAC03431.1; -; mRNA.  
DR HSP: Q12967; 2RGF.  
DR Ensembl: ENSG00000160271; Homo sapiens.  
DR GO: GO:0005085; F:guanylyl-nucleotide exchange factor activity; IEA.  
DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.  
DR InterPro: IPR001895; RasGRF\_CDC25.  
DR Pfam: PF00617; RasGEF; 1.  
DR SMART: SM00147; RasGEF; 1.  
DR PROSITE: PS00720; RasGEF; 1.  
DR PROSITE: PS50009; RasGEF\_CAT; 1.  
FT NON TER 1 1  
SQ SEQUENCE 745 AA; 81765 MW; 3A2330D768EE6E7D CRC64;  
  
Query Match 2.4%; Score 17; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 421 VPIYGTFLTDLVMLDPTA 437  
Db 360 VPIYGTFLTDLVMLDPTA 376  
  
RESULT 14  
O8TEK9\_HUMAN PRELIMINARY; PRT; 824 AA.  
AC O8TEK9;  
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2002, sequence version 1.  
DT 07-FEB-2006, entry version 14.  
DE FLJ00185 protein (Fragment).  
GN Name=FLJ00185;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;

FT NON TER 1 1  
SQ SEQUENCE 625 AA; 68192 MW; 9PFC16C867F54561 CRC64;  
  
Query Match 2.4%; Score 17; DB 2; Length 625;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 421 VPIYGTFLTDLVMLDPTA 437  
Db 353 VPIYGTFLTDLVMLDPTA 369  
  
RESULT 13  
O9P2N8\_HUMAN PRELIMINARY; PRT; 745 AA.  
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DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2000, sequence version 1.  
DT 07-FEB-2006, entry version 17.  
DE KIAA1308 protein (Fragment).  
GN Name=KIAA1308;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=20181126; PubMed=10718198; DOI=10.1093/dnares/7.1.65;  
RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XVI.  
RT The complete sequences of 150 new cDNA clones from brain which code  
RT for large proteins in vitro";  
RL DNA Res. 7:65-73(2000).  
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CC -----  
CC EMBL: AB037729; BAA92546.1; -; mRNA.  
DR GO: GO:0005085; F:guanylyl-nucleotide exchange factor activity; IEA.  
DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.  
DR InterPro: IPR001895; RasGRF\_CDC25.  
DR Pfam: PF00617; RasGEF; 1.  
DR SMART: SM00147; RasGEF; 1.  
DR PROSITE: PS00720; RasGEF; 1.  
DR PROSITE: PS50009; RasGEF\_CAT; 1.  
FT NON TER 1 1  
SQ SEQUENCE 745 AA; 81765 MW; 3A2330D768EE6E7D CRC64;  
  
Query Match 2.4%; Score 17; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 421 VPIYGTFLTDLVMLDPTA 437  
Db 360 VPIYGTFLTDLVMLDPTA 376  
  
RESULT 14  
O8TEK9\_HUMAN PRELIMINARY; PRT; 824 AA.  
AC O8TEK9;  
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2002, sequence version 1.  
DT 07-FEB-2006, entry version 14.  
DE FLJ00185 protein (Fragment).  
GN Name=FLJ00185;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
 RC NUCLEOTIDE SEQUENCE.  
 RA Tissue-Spleen:  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: AK074114; BAB94940.1; -; mRNA.  
 DR HSP: Q12967; 2RGF.  
 DR Ensembl: ENSG00000160271; Homo sapiens.  
 DR GO: GO:0005085; P:guanylyl-nucleotide exchange factor activity; IEA.  
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.  
 DR InterPro: IPR000651; Rasgef N.  
 DR InterPro: IPR001895; RasGRF\_CDC5.  
 DR Pfam: PF00617; Rasgef 1.  
 DR Pfam: PF00618; Rasgef N; 1.  
 DR SMART: SM00147; Rasgef; 1.  
 DR SMART: SM00229; RasgefN; 1.  
 DR PROSITE: PS00720; Rasgef; 1.  
 DR PROSITE: PS00009; Rasgef CAT; 1.  
 DR PROSITE: PS0212; Rasgef-INTER; 1.  
 FT NON\_TER 1 1  
 SO SEQUENCE 824 AA; 90263 MW; EFBB582CADF8FA26 CRC64;  
 Query Match 2.4%; Score 17; DB 2; Length 824;  
 Best Local Similarity 100.0%; Pred.No.16e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 421 VPLYGTFLLDVLMDTA 437  
 Db 552 VPLYGTFLLDVLMDTA 568  
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RESULT 15  
 Q3UQY9 MOUSE PRELIMINARY; PRT; 840 AA.  
 ID Q3UQY9  
 AC Q3UQY9  
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.  
 DT 11-OCT-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DE 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched  
 DE library, clone: D130075H07 product: rat guanine nucleotide dissociation  
 DE stimulator; full insert sequence.  
 GN Name=Ralgds;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Mus.  
 OC NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; Tissue=Spinal ganglion;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carinini P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RL Methods Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; Tissue=Spinal ganglion;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carinini P., Kasukawa T., Katayama S., Gough J., Fitch M.C., Maeda N.,  
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzhus R., Shimokawa K.,  
 Baisic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
 Davis M.J., Wilming L.G., Aldins V., Allen J.E.,  
 RA Amesel-Imbolcato A., Apweiler R., Atturliya R.N., Bailey T.L.,  
 Bamsel M.J., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
 Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,

RA Gusfincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 Hill D., Hummel L., Iacono M., Ieko K., Iwama A., Ishikawa T.,  
 Jakt M., Kamitani A., Katoh M., Kawasawa Y., Keiso J., Kitamura H.,  
 Kitano H., Kollis G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 Liuti S., McWilliam S., Madan Babu M., Mader A., Marchionni L.,  
 Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 Mortagu-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,  
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 Okazaki Y., Orlando V., Pang K.C., Pavan M.J., Pavoni G., Pesole G.,  
 Petrovsky N., Plaza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
 Roost B., Ruan Y., Salzberg S.L., Sander A., Schneider C.,  
 Schonbach C., Sekiguchi K., Semple C.A., Sessa L., Sheng Y.,  
 Shihata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K.,  
 Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeag K.,  
 Yamashita H., Zdobovskiy E., Zhu S., Zimmer A., Hide W., Bult C.,  
 Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 Wahlestedt C., Matlock J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimura N.,  
 Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome";  
 RL Science 309:1559-1563(2005).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; Tissue=Spinal ganglion;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 RG (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense transcription in the mammalian transcriptome";  
 RL Science 309:1564-1566(2005).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; Tissue=Spinal ganglion;  
 RX MEDLINE=22554683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,  
 Okazaki Y., Osato N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Haegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Balarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gusfincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kongsaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Nunata K., Okita T., Pavan W.J., Petrea G., Pesole G.,  
 RA Petrovsky N., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Serou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carinini P., Hayashizaki Y.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shigaawa A.,  
 RA Yasunishi A., Yoshino Y.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; Tissue=Spinal ganglion;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Atzawa K., Irawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,  
 RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schiraldi L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Mashin T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereys P.,  
 RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,  
 RA Hayashizaki Y.,  
 RA "Functional annotation of a full-length mouse cDNA collection.";  
 RT Nature 409:685-690(2001).  
 RL [6]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RC MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [7]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RC MEDLINE=20530913; PubMed=11076863; DOI=10.1101/gr.152600;  
 RX Shibata K., Itoh M., Atzawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Irawa M., Ohara E., Watabiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN Integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [8]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RC Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
 RA Horii F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,  
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,  
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watabiki A.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL: AK141959; BAR24899.1; -; mRNA.  
 DR MGI: 107485; RA1908.  
 DR GO: GO:0008289; F:lipid binding; RCA.  
 DR GO: GO:0005515; F:protein binding; IPI.  
 DR GO: GO:0006810; P:transport; RCA.  
 DR InterPro: IPR000159; RA.  
 DR InterPro: IPR000651; Rasgef N.  
 DR InterPro: IPR001895; Rasgef CDC25.  
 DR Pfam: PF00788; RA; 1.  
 DR Pfam: PF00617; Rasgef; 1.  
 DR Pfam: PF00618; Rasgef N; 1.  
 DR SMART: SM00314; RA; 1.  
 DR SMART: SM00147; Rasgef; 1.  
 DR SMART: SM00229; Rasgef N; 1.  
 DR PROSITE: PS50200; RA; 1.  
 DR PROSITE: PS00720; Rasgef; 1.

DR PROSITE: PS50009; Rasgef CAT; 1.  
 DR PROSITE: PS50212; Rasgef NTER; 1.  
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 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 421 VPTLGTFLDVLVMDTA 437  
 DB 490 VPTLGTFLDVLVMDTA 506

Search completed: June 12, 2006, 12:04:38  
 Job time : 308 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 12, 2006, 11:59:50 ; Search time 44 Seconds  
(without alignments)  
1552.589 Million cell updates/sec

Title: US-10-694-438-2

Perfect score: 710

Sequence: 1 MERTAGKELALAPLDWGEE.....RDFMLRKEGTRNTLSVSPS 710

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80.\*

1: .pir1.\*

2: .pir2.\*

3: .pir3.\*

4: .pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	2.4	852	S28415	guanine nucleotide
2	11	1.5	754	T12453	hypothetical prote
3	11	1.5	768	A56234	ral guanine nucleo
4	10	1.4	328	I38853	guanine nucleotide
5	10	1.4	842	T16198	hypothetical prote
6	9	1.3	94	PC4379	Rif. RalGDS-like f
7	9	1.3	132	H96708	hypothetical prote
8	9	1.3	150	C85799	dATP pyrophospho
9	9	1.3	150	G90950	dATP pyrophospho
10	9	1.3	150	B38113	dATP pyrophospho
11	9	1.3	438	AF0068	UDP-N-acetylmuram
12	9	1.3	502	A55197	Wiskott-Aldrich sy
13	9	1.3	777	T08659	ral guanine nucleo
14	9	1.3	2048	1 ZLNZSE	genome polypote
15	9	1.3	2228	1 ZLNZSV	genome polypote
16	8	1.1	152	A83574	hypothetical prote
17	8	1.1	192	T30477	hypothetical prote
18	8	1.1	232	AC2774	DNA repair prote
19	8	1.1	248	1 TVMVR5	transforming prote
20	8	1.1	288	T12462	hypothetical prote
21	8	1.1	305	A97554	DNA repair prote
22	8	1.1	379	2 T19069	hypothetical prote
23	8	1.1	388	JC5437	spliceosome-associ
24	8	1.1	446	2 T24958	hypothetical prote
25	8	1.1	449	2 J01438	polyprotein - tuli
26	8	1.1	550	2 G70597	probable proteinase
27	8	1.1	611	1 S62811	oligodehydrogenase
28	8	1.1	627	2 H86180	hypothetical prote
29	8	1.1	632	2 S38042	probable purine nu

30	8	1.1	644	2 T33132	hypothetical prote
31	8	1.1	696	2 A12849	GGDEF family prote
32	8	1.1	696	2 G97626	hypothetical prote
33	8	1.1	753	2 B36268	platelet glycoprot
34	8	1.1	778	2 A60798	platelet glycoprot
35	8	1.1	788	2 A26547	platelet glycoprot
36	8	1.1	788	2 I77349	platelet glycoprot
37	8	1.1	797	2 S53590	hypothetical prote
38	8	1.1	851	2 T47305	hypothetical prote
39	8	1.1	909	2 S32538	cGMP-gated cation
40	8	1.1	1002	2 I56963	transposase - Esch
41	8	1.1	1018	2 JC4211	neural adhesion pr
42	8	1.1	1039	2 F71427	hypothetical prote
43	8	1.1	1144	2 T25765	hypothetical prote
44	8	1.1	1201	2 A57369	anillin - fruit fl
45	8	1.1	1329	2 E70917	hypothetical glyci

ALIGNMENTS

RESULT 1

S28415  
guanine nucleotide dissociation stimulator ralGDS - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004  
A:Accession: S28415  
R:Albright, C.F.; Giddings, B.W.; Liu, J.; Vito, M.; Weinberg, R.A.  
EMBO J. 12, 339-347, 1993  
A:Title: Characterization of a guanine nucleotide dissociation stimulator for a ras-rel  
A:Reference number: S28415; MUID:93154339; PMID:8094051  
A:Accession: S28415  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-852 <ALB>  
A:Cross-references: UNIPROT:Q03385; UNIPARC:UPI0000029858; GB:I07924; NID:ig193572; PIDN  
F:320-586/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

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Best Local Similarity 100.0%; Pred. No. 9.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 421 VPYLGTFLTDLVMLDTA 437  
Db 502 VPYLGTFLTDLVMLDTA 518

RESULT 2

T12453  
hypothetical protein DKFZp564D2123.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, June 1999  
A:Reference number: Z17524  
A:Accession: T12453  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-754 <WAM>  
A:Cross-references: UNIPROT:Q9NZL6; UNIPARC:UPI000016AC59; EMBL:AL080117  
A:Experimental source: fetal brain; clone DKFZp564D2123  
C:Genetics:  
A>Note: DKFZp564D2123.1  
F:1214-487/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match 1.5%; Score 11; DB 2; Length 754;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 421 VPYLGTFLTDL 431  
Db 403 VPYLGTFLTDL 413

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A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2
F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match      1:4%; Score 10; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 446 LINFEKRRKE 455
Db 422 LINFEKRRKE 431

RESULT 6
PC4379
Rlf, RalGDS-like factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Nov-1997 #sequence_revision 06-Nov-1997 #text_change 07-May-1999
C;Accession: PC4379
R;O'Gara, M.J.; Zhang, X.; Baker, L.; Marshall, M.S.
Biochem. Biophys. Res. Commun. 238, 425-429, 1997
A;Title: Characterization of the Ras binding domain of the RalGDS-related protein, RLF.
A;Reference number: PC4379; MUID:97445998; PMID:9299525
A;Accession: PC4379
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-94 <OAG>
A;Cross-references: UNIPARC:UPI000017C73F
C;Comment: This protein belongs to RalGDS family which are guanine-nucleotide exchange

Query Match      1.3%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 635 TSQDKAPSV 643
Db 29 TSQDKAPSV 37

RESULT 7
H96708
hypothetical protein T26J14.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H96708
R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96708
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <STO>
A;Cross-references: UNIPROT:Q9CA33; UNIPARC:UPI00000A1CA4; GB:AE005173; NID:96553937; P
C;Genetics:
A;Gene: T26J14.5
A;Map position: 1

Query Match      1.3%; Score 9; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 PPMPPPPPP 123
Db 15 PPMPPPPPP 23

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F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match      1:4%; Score 10; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 446 LINFEKRRKE 455
Db 422 LINFEKRRKE 431

RESULT 6
PC4379
Rlf, RalGDS-like factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Nov-1997 #sequence_revision 06-Nov-1997 #text_change 07-May-1999
C;Accession: PC4379
R;O'Gara, M.J.; Zhang, X.; Baker, L.; Marshall, M.S.
Biochem. Biophys. Res. Commun. 238, 425-429, 1997
A;Title: Characterization of the Ras binding domain of the RalGDS-related protein, RLF.
A;Reference number: PC4379; MUID:97445998; PMID:9299525
A;Accession: PC4379
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-94 <OAG>
A;Cross-references: UNIPARC:UPI000017C73F
C;Comment: This protein belongs to RalGDS family which are guanine-nucleotide exchange

Query Match      1.3%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 635 TSQDKAPSV 643
Db 29 TSQDKAPSV 37

RESULT 7
H96708
hypothetical protein T26J14.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H96708
R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96708
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <STO>
A;Cross-references: UNIPROT:Q9CA33; UNIPARC:UPI00000A1CA4; GB:AE005173; NID:96553937; P
C;Genetics:
A;Gene: T26J14.5
A;Map position: 1

Query Match      1.3%; Score 9; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 PPMPPPPPP 123
Db 15 PPMPPPPPP 23

A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2
F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match      1.5%; Score 11; DB 2; Length 768;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 421 VPYLGTFELTDL 431
Db 417 VPYLGTFELTDL 427

RESULT 4
I38853
guanine nucleotide dissociation stimulator ralGDS - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C;Accession: I38853
R;Hofer, F.; Fields, S.; Schneider, C.; Martin, G.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 11089-11093, 1994
A;Title: Activated Ras interacts with the Ral guanine nucleotide dissociation stimulator
A;Reference number: I38853; MUID:95062211; PMID:7972015
A;Accession: I38853
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-328 <RES>
A;Cross-references: UNIPROT:Q12967; UNIPARC:UPI000016A11C; EMBL:U14417; NID:9538199; PID
F;1-62/Domain: CDC25-type guanine nucleotide exchange activator homology (fragment) <SOS>

Query Match      1.4%; Score 10; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 446 LINFEKRRKE 455
Db 3 LINFEKRRKE 12

RESULT 5
T16198
hypothetical protein F28B4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16198
R;Leimbach, D.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F28B4.
A;Reference number: Z18475
A;Accession: T16198
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-842 <LEI>
A;Cross-references: UNIPROT:Q19852; UNIPARC:UPI000001B947; EMBL:U42834; NID:g1125756; PID
C;Genetics:
A;Gene: CESP:F28B4.2

```

## RESULT 8

cdATP pyrophosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain EDL93)  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004  
 C:Accession: C85799  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: C85799  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-150 <STO>  
 A:Cross-references: UNIPROT:P24236; UNIPARC:UPI00001308E5; GB:AE005174; NID:g12515921; F  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: Z2917

Query Match 1.3%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 VAEQLTLID 259  
 |||||  
 Db 66 VAEQLTLID 74

## RESULT 9

cdATP pyrophosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain RMD  
 G90950  
 C:Species: Escherichia coli  
 C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 05-Oct-2004  
 C:Accession: G90950  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
 A:Reference number: A99629; MUID:21156231; PMID:11358796  
 A:Accession: G90950  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-150 <HAY>  
 A:Cross-references: UNIPROT:P24236; UNIPARC:UPI00001308E5; GB:BA000007; PIDN:BA035998.1;  
 A:Experimental source: strain O157:H7, substrain RMD 050952  
 C:Genetics:  
 A:Gene: EC2575

Query Match 1.3%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 VAEQLTLID 259  
 |||||  
 Db 66 VAEQLTLID 74

## RESULT 10

cdATP pyrophosphohydrolase (EC 3.6.1.-) - Escherichia coli (strain K-12)  
 B38113  
 C:Species: Escherichia coli  
 C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 31-Dec-2004  
 C:Accession: B38113; S19013; A64949  
 R:Takahagi, M.; Iwasaki, H.; Nakata, A.; Shinagawa, H.  
 J. Bacteriol. 173, 5747-5753, 1991  
 A:Title: Molecular analysis of the Escherichia coli ruvC gene, which encodes a Holliday  
 A:Reference number: A38113; MUID:91358366; PMID:1885548  
 A:Accession: B38113  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-150 <TAK>  
 A:Cross-references: UNIPROT:P24236; UNIPARC:UPI00001308E5; GB:D10165; GB:D90392; NID:g2U

R:Sharples, G.J.; Lloyd, R.G.  
 J. Bacteriol. 173, 7711-7715, 1991  
 A:Title: Resolution of Holliday junctions in Escherichia coli: identification of the ru  
 A:Reference number: S19013; MUID:92041688; PMID:1657895  
 A:Accession: S19013  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-150 <SHA>  
 A:Cross-references: UNIPARC:UPI00001308E5; EMBL:X59551; NID:g42172; PIDN:CAA42124.1; PI  
 A:Experimental source: strain K-12  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C  
 .A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: A64949  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-150 <BLAT>  
 A:Cross-references: UNIPARC:UPI00001308E5; GB:AE000280; GB:U00096; NID:g1788163; PIDN:AJ  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Genetics:  
 A:Gene: ntpA  
 C:Keywords: hydrolase  
 F:36-70/Domain: mutT domain homology <MUTT>

Query Match 1.3%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 VAEQLTLID 259  
 |||||  
 Db 66 VAEQLTLID 74

## RESULT 11

AF0068  
 UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9) [imported] - Yersinia pestis  
 C:Species: Yersinia pestis  
 C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C:Accession: AF0068  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
 Nature 413, 523-527, 2001  
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360  
 A:Accession: AF0068  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-438 <KUR>  
 A:Cross-references: UNIPROT:Q8ZIF1; UNIPARC:UPI00000DC8F9; GB:AL590842; PIDN:CAC89409.1;  
 C:Genetics:  
 A:Gene: murD  
 C:Superfamily: UDP-N-acetylmuramate-alanine ligase  
 C:Keywords: ligase

Query Match 1.3%; Score 9; DB 2; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 3.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 666 VLPQDRVLL 674  
 |||||  
 Db 402 VLPQDRVLL 410

## RESULT 12

A55197  
 Wiskott-Aldrich syndrome protein WASP - human  
 C:Species: Homo sapiens (man)  
 C:Date: 23-Mar-1995 #sequence\_revision 24-Nov-1999 #text\_change 09-Jul-2004  
 C:Accession: A54747; A55197; I38931  
 R:Derry, J.M.J.; Ochs, H.D.; Francke, U.

```
Cell 78, 635-644, 1994
A:Title: Isolation of a novel gene mutated in Wiskott-Aldrich syndrome.
A:Reference number: A54747; MUID:9439367; PMID:8069912
A:Accession: A54747
A:Molecule type: mRNA
A:Residues: 1-328, 'A', 330-366, 'LHHPLQLLDVLDHCPLELVGHPCHH', 'HRRHRRPAPGMDQPLPHSLLLWC
A:Cross-references: UNIPROT:P42768; UNIPARC:UPI000017C421; GB:U12707
A>Note: this sequence is corrected in reference A55197
R:Derry, J.M.J.; Ochs, H.D.; Francke, U.
Cell 79, 922a, 1994
A:Reference number: A55197
A:Contents: erratum
A:Accession: A55197
A:Molecule type: mRNA
A:Residues: 1-424, 'PG', 427-502 <DER>
A:Cross-references: UNIPARC:UPI000017C422; GB:U12707; NID:9695150
A>Note: the translated sequence in GenBank entry HSU12707 (PIDN:AAA62663.1) differs from
R:Kwan, S.P.; Hagemann, T.L.; Radtke, B.E.; Blaese, R.M.; Rosen, F.S.
Proc. Natl. Acad. Sci. U.S.A. 92, 4706-4710, 1995
A:Title: Identification of mutations in the Wiskott-Aldrich syndrome gene and characteri
A:Reference number: I38931; MUID:95273432; PMID:7753869
A:Accession: I38931
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <KWA>
A:Cross-references: UNIPARC:UPI000003CRA0; EMBL:U19927; NID:9854672; PIDN:AAC50140.1; PI
C:Genetics:
A:Gene: GDB:WAS; IMD2; WASP
A:Cross-references: GDB:120736; OMIM:301000
A:Map position: Xp11.23-Xp11.22
A>Note: defects in this gene may result in Wiskott-Aldrich syndrome
C:Keywords: immunodeficiency

Query Match 1.3%; Score 9; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 PMPMPPPPP 123
Db 391 PMPMPPPPP 399

RESULT 13
T08659
ral guanine nucleotide dissociation stimulator-like protein RGL2 - human
N:Alternate names: protein DKF2p547D0710.1; RalGDS-like factor RGL2
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08659
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16466
A:Accession: T08659
A:Molecule type: mRNA
A:Residues: 1-777 <POU>
A:Cross-references: UNIPROT:O15211; UNIPARC:UPI0000001621; EMBL:AL050259
A:Experimental source: fetal brain; clone DKF2p547D0710
C:Genetics:
A>Note: DKF2p547D0710.1
C:Function:
A:Description: probably involved in Ras-mediated cellular transformation
P:239-513/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match 1.3%; Score 9; DB 2; Length 777;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 TSQDKAPSV 643
Db 671 TSQDKAPSV 679

RESULT 14
```

```
ZLNZSE
genome polyprotein - Sendai virus (strain Enders)
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: Sendai virus
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A24293
R:Morgan, E.M.; Rakestraw, K.M.
Virology 154, 31-40, 1986
A:Title: Sequence of the Sendai virus L gene: open reading frames upstream of the main c
A:Reference number: A24293; MUID:86317720; PMID:3019006
A:Accession: A24293
A:Molecule type: genomic RNA
A:Residues: 1-2048 <MOR>
A:Cross-references: UNIPROT:P06829; UNIPARC:UPI0000134AF9; GB:M14887; NID:G334975; PIDN
C:Genetics:
A:Gene: L
C:Superfamily: parainfluenza virus RNA-directed RNA polymerase
C:Keywords: ATP; nucleotidyltransferase

Query Match 1.3%; Score 9; DB 1; Length 2048;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 DLELFKVR 267
Db 1230 DLELFKVR 1238

RESULT 15
ZLNZSV
genome polyprotein - Sendai virus (strain Z)
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: Sendai virus
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A04120
R:Shioda, T.; Iwasaki, K.; Shibuta, H.
Nucleic Acids Res. 14, 1545-1563, 1986
A:Title: Determination of the complete nucleotide sequence of the Sendai virus genome R
A:Reference number: A00878; MUID:86148492; PMID:3005975
A:Accession: A04120
A:Molecule type: genomic RNA
A:Residues: 1-2228 <SHI>
A:Cross-references: UNIPROT:P06447; UNIPARC:UPI0000134AFB; GB:X03614; NID:960898; PIDN:
C:Genetics:
A:Gene: L
C:Superfamily: parainfluenza virus RNA-directed RNA polymerase
C:Keywords: ATP; nucleotidyltransferase

Query Match 1.3%; Score 9; DB 1; Length 2228;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 DLELFKVR 267
Db 1410 DLELFKVR 1418

Search completed: June 12, 2006, 12:05:27
Job time : 47 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: June 12, 2006, 12:16:58 ; Search time 181 Seconds  
(without alignments)  
1817.031 Million cell updates/sec

Title: US-10-694-438-2  
Perfect score: 710  
Sequence: 1 MERTAGKELALAPLQDWGEE.....RDFMLRRKRGTRNTLSVSPS 710  
Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 2097797 seqs, 463214858 residues

Word size : 1  
Total number of hits satisfying chosen parameters: 2096646  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Listing first 45 summaries

Database : Published Applications AA\_Main:  
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5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the change being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	710	100.0	710	4	US-10-118-328-2
2	710	100.0	710	4	US-10-694-438-2
3	609	85.8	710	4	US-10-060-990-3
4	609	85.8	710	4	US-10-287-218-9
5	609	85.8	710	4	US-10-474-291-9
6	609	85.8	710	5	US-10-894-680A-3
7	487	68.6	715	3	US-09-808-701A-33
8	487	68.6	715	4	US-10-233-131-33
9	487	68.6	715	4	US-10-240-145-85
10	487	68.6	715	5	US-10-291-128-85
11	449	63.2	699	3	US-09-808-701A-34
12	449	63.2	699	4	US-10-233-131-34
13	449	63.2	699	4	US-10-240-145-86
14	449	63.2	699	5	US-10-291-128-86
15	435	61.3	464	4	US-10-094-749-2959
16	381	53.7	708	4	US-10-074-978A-76
17	264	37.2	264	5	US-10-894-680A-60
18	261	36.8	261	4	US-10-074-978A-336
19	211	29.7	211	4	US-10-074-978A-338
20	207	29.2	208	4	US-10-108-260A-3953
21	100	14.1	135	5	US-10-894-680A-55
22	87	12.3	87	5	US-10-894-680A-65
23	73	10.3	75	4	US-10-074-978A-344
24	56	7.9	83	4	US-10-074-978A-342
25	48	6.8	70	3	US-09-864-761-40158
26	47	6.6	343	4	US-10-074-978A-333
27	47	6.6	343	4	US-10-074-978A-334

28	47	6.6	709	4	US-10-118-328-4	Sequence 4, Appli
29	47	6.6	709	4	US-10-074-978A-332	Sequence 332, App
30	47	6.6	709	4	US-10-074-978A-335	Sequence 335, App
31	47	6.6	709	4	US-10-694-438-4	Sequence 4, Appli
32	20	2.8	20	4	US-10-060-990-5	Sequence 5, Appli
33	20	2.8	20	5	US-10-894-680A-5	Sequence 5, Appli
34	17	2.4	268	5	US-10-894-680A-62	Sequence 62, Appli
35	17	2.4	677	4	US-10-103-313-384	Sequence 384, App
36	17	2.4	824	5	US-10-719-993-797	Sequence 797, App
37	17	2.4	847	5	US-10-719-993-798	Sequence 798, App
38	17	2.4	886	5	US-10-719-993-799	Sequence 799, App
39	17	2.4	902	3	US-09-922-199A-2	Sequence 2, Appli
40	17	2.4	914	5	US-10-719-993-800	Sequence 800, App
41	17	2.4	953	5	US-10-719-993-796	Sequence 796, App
42	11	1.5	119	3	US-09-922-199A-12	Sequence 12, Appl
43	11	1.5	140	3	US-09-922-199A-11	Sequence 11, Appl
44	11	1.5	193	4	US-10-103-313-304	Sequence 304, App
45	11	1.5	725	4	US-10-118-328-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-10-118-328-2  
; Sequence 2, Application US/10118328  
; Publication No. US20020169289A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE  
; FILE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL001220  
; CURRENT APPLICATION NUMBER: US/10/118.328  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/282,460  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-118-328-2

Query Match		100.0%	Score 710;	DB 4;	Length 710;
Best Local Similarity		100.0%	Pred. No. 0;		
Matches 710;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MERTAGKELALAPLQDWGEEETDGA	VYSVLSRRQRSSPAEGGSOAPS	PIANTFLH	60
Db	1	MERTAGKELALAPLQDWGEEETDGA	VYSVLSRRQRSSPAEGGSOAPS	PIANTFLH	60
QY	61	YRTSKRVLRARLERLVGELVFGD	REDDPSFMFAFLATYTFVTAC	LLGFLPPMPP	120
Db	61	YRTSKRVLRARLERLVGELVFGD	REDDPSFMFAFLATYTFVTAC	LLGFLPPMPP	120
QY	121	PPGVEIKKTAVQDLSFNKNLR	AVVSVLGSWLQDHPQDRDHP	VHSDLSGVRTFLGWAAP	180
Db	121	PPGVEIKKTAVQDLSFNKNLR	AVVSVLGSWLQDHPQDRDHP	VHSDLSGVRTFLGWAAP	180
QY	181	GSAAQKAEKLLDPLEEAEREQEE	EPQVWTPPVRAQTSDDPSSE	ACAEEEGLMPQG	240
Db	181	GSAAQKAEKLLDPLEEAEREQEE	EPQVWTPPVRAQTSDDPSSE	ACAEEEGLMPQG	240
QY	241	PQLDFFSDEVAEQTLTDLFLSK	VRLYECLGVSWSQDRPGAAG	ASPTVRATVAQNT	300
Db	241	PQLDFFSDEVAEQTLTDLFLSK	VRLYECLGVSWSQDRPGAAG	ASPTVRATVAQNT	300
QY	301	VTGCVLSGLCAPGAAAPQRAOR	LEKWRIRIAQRCELNFSSRA	ILSALQSNPIYRLKR	360
Db	301	VTGCVLSGLCAPGAAAPQRAOR	LEKWRIRIAQRCELNFSSRA	ILSALQSNPIYRLKR	360

QY 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLPSKPPGP 420  
DB 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLPSKPPGP 420  
QY 421 VPYLGTFELTDVMDLTALPDMLDGLINFEKRRKWEILARIQOLQRRCSYTLSPHPPI 480  
DB 421 VPYLGTFELTDVMDLTALPDMLDGLINFEKRRKWEILARIQOLQRRCSYTLSPHPPI 480  
QY 481 LAALHAQNQLTEEQSYRLSRVIEPPAASCPSRRIRRIISLTKLSAKLAREKSSSPSGS 540  
DB 481 LAALHAQNQLTEEQSYRLSRVIEPPAASCPSRRIRRIISLTKLSAKLAREKSSSPSGS 540  
QY 541 PGDPSSPTSSVSPGSPSSPRSDAPAGSPGPGQSTKPLSLDLSPRPFPALPLG 600  
DB 541 PGDPSSPTSSVSPGSPSSPRSDAPAGSPGPGQSTKPLSLDLSPRPFPALPLG 600  
QY 601 SPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNPQWACD 660  
DB 601 SPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNPQWACD 660  
QY 661 YQLFQVLPGRVLLIPDNANVFAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
DB 661 YQLFQVLPGRVLLIPDNANVFAMSPVAPRDFMLRKEGTRNTLSVSPS 710

RESULT 2  
US-10-694-438-2  
; Sequence 2, Application US/10694438  
; Publication No. US20040142352A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE  
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL001220-DIV  
; CURRENT APPLICATION NUMBER: US/10/694,438  
; PRIOR FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: 10/118,328  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/282,460  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-694-438-2

Query Match 100.0%; Score 710; DB 4; Length 710;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERTAGKELALAPLQDWGEETEGAVYSVLRQRQRSPAGPGGSOAPSPIANTFLH 60  
DB 1 MERTAGKELALAPLQDWGEETEGAVYSVLRQRQRSPAGPGGSOAPSPIANTFLH 60  
QY 61 YRTSKVRVLAARLERLVGELVFGDREDDPSFMPAFIATYRTFVTACLLGFLLPMPPP 120  
DB 61 YRTSKVRVLAARLERLVGELVFGDREDDPSFMPAFIATYRTFVTACLLGFLLPMPPP 120  
QY 121 PPGVEIKKTAVQDLGFNKNLRAVSVLGSWLQDHPQDFRDHPVSDLSGVRFTFLGWAAP 180  
DB 121 PPGVEIKKTAVQDLGFNKNLRAVSVLGSWLQDHPQDFRDHPVSDLSGVRFTFLGWAAP 180  
QY 181 GSAEAKAEKLLDEFTLEAEAREEPPQVWTGPPRAVQTSDDPSSEACAEDEEGLMPOG 240  
DB 181 GSAEAKAEKLLDEFTLEAEAREEPPQVWTGPPRAVQTSDDPSSEACAEDEEGLMPOG 240  
QY 241 PQLLDFSVDEVAEQTLIDLELFSKVLRYECLGSVMSQRDRPCAAGASPTVRATVAQFNT 300  
DB 241 PQLLDFSVDEVAEQTLIDLELFSKVLRYECLGSVMSQRDRPCAAGASPTVRATVAQFNT 300

QY 301 VTGCVLGSVLGAPGLAAAPQARLEKWIRIAQRCRELRFSSRLAISALQSNPIYRLKR 360  
DB 301 VTGCVLGSVLGAPGLAAAPQARLEKWIRIAQRCRELRFSSRLAISALQSNPIYRLKR 360  
QY 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLPSKPPGP 420  
DB 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLPSKPPGP 420  
QY 421 VPYLGTFELTDVMDLTALPDMLDGLINFEKRRKWEILARIQOLQRRCSYTLSPHPPI 480  
DB 421 VPYLGTFELTDVMDLTALPDMLDGLINFEKRRKWEILARIQOLQRRCSYTLSPHPPI 480  
QY 481 LAALHAQNQLTEEQSYRLSRVIEPPAASCPSRRIRRIISLTKLSAKLAREKSSSPSGS 540  
DB 481 LAALHAQNQLTEEQSYRLSRVIEPPAASCPSRRIRRIISLTKLSAKLAREKSSSPSGS 540  
QY 541 PGDPSSPTSSVSPGSPSSPRSDAPAGSPGPGQSTKPLSLDLSPRPFPALPLG 600  
DB 541 PGDPSSPTSSVSPGSPSSPRSDAPAGSPGPGQSTKPLSLDLSPRPFPALPLG 600  
QY 601 SPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNPQWACD 660  
DB 601 SPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNPQWACD 660  
QY 661 YQLFQVLPGRVLLIPDNANVFAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
DB 661 YQLFQVLPGRVLLIPDNANVFAMSPVAPRDFMLRKEGTRNTLSVSPS 710

RESULT 3  
US-10-060-990-3  
; Sequence 3, Application US/10060990  
; Publication No. US20030032159A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Nguyen, Cung-Tuong  
; TITLE OF INVENTION: HUMAN RALGDS-LIKE PROTEIN 3  
; FILE REFERENCE: PB0176  
; CURRENT APPLICATION NUMBER: US/10/060,990  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/326,105  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 3  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-060-990-3

Query Match 85.8%; Score 609; DB 4; Length 710;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MERTAGKELALAPLQDWGEETEGAVYSVLRQRQRSPAGPGGSOAPSPIANTFLH 60

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Db 1 MERTAGKELALAPLDQWGEETEDGAVYSVLSRRQSRQSPAEQSGQAPSPANTFLH 60
Qy 61 YRTSKVRVLAARLERLVLGDEQDQSPFAFLATYRTFVPTACLLGFLLLPMPPP 120
Db 61 YRTSKVRVLAARLERLVLGDEQDQSPFAFLATYRTFVPTACLLGFLLLPMPPP 120
Qy 121 PPPGVEIKTAVQDLSPFNKRLRAVSVLGSWLDQHPQDFRDHPVHSDLGSVRTFLGWAAP 180
Db 121 PPPGVEIKTAVQDLSPFNKRLRAVSVLGSWLDQHPQDFRDHPVHSDLGSVRTFLGWAAP 180
Qy 181 GSAAQAKAEKLLDFLEAEAREQEEPPQVMTGPRVAQTSDDPSSEACAEBEGLMPOG 240
Db 181 GSAAQAKAEKLLDFLEAEAREQEEPPQVMTGPRVAQTSDDPSSEACAEBEGLMPOG 240
Qy 241 POLDFSDEVAEQTLIDLEFSKRVLYECLGSVMSQDRDRPAAAGASPTVATVAQFNT 300
Db 241 POLDFSDEVAEQTLIDLEFSKRVLYECLGSVMSQDRDRPAAAGASPTVATVAQFNT 300
Qy 301 VTGCVLGSVLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSRLAILSLAQSNPIYRLKR 360
Db 301 VTGCVLGSVLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSRLAILSLAQSNPIYRLKR 360
Qy 361 SWGAVSREPLSTFRKLSQIFSDNNHLSGREILFQEEATEGSEEDNTPGSLPSKPPGP 420
Db 361 SWGAVSREPLSTFRKLSQIFSDNNHLSGREILFQEEATEGSEEDNTPGSLPSKPPGP 420
Qy 421 VPYLGTFTLDVMDLTPALPDMLGDLINFEKRWKEWILLARIOQORRCQSYLSHPPI 480
Db 421 VPYLGTFTLDVMDLTPALPDMLGDLINFEKRWKEWILLARIOQORRCQSYLSHPPI 480
Qy 481 LAALHAQNLTEQSYRLSVIEPPAAACPSPPRRIRRLSLTKLSAKLAREKSSPSGS 540
Db 481 LAALHAQNLTEQSYRLSVIEPPAAACPSPPRRIRRLSLTKLSAKLAREKSSPSGS 540

RESULT 4
US-10-287-218-9
; Sequence 9, Application US/10287218
; Publication No. US20030198975A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: AZIMZAI, Valda; AU-YOUNG, Janice K.
; APPLICANT: BATRA, Sajeev; BAUGHN, Mariah R.
; APPLICANT: BECHA, Shanya D.; BOROWSKY, Mark L.
; APPLICANT: BUFORD, Neil; DING, Li
; APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.
; APPLICANT: GANDHI, Ameena R.; GIETZEN, Kimberly J.
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.
; APPLICANT: HONCHELL, Cynthia D.; LAL, Preeti G.
; APPLICANT: LEE, Soo Yeun; LU, Dzung Aina M.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: REDDY, Roopa; SANJANWALA, Madhu, M.
; APPLICANT: TANG, Y. Tom; WALIA, Narinder K.
; APPLICANT: WANG, Yu-mei, E.; WARREN, Bridget A.
; APPLICANT: XU, Yuming; YANG, Junning
; APPLICANT: YAO, Monique G.; YUE, Henry
; APPLICANT: ZEBARJADIAN, Yeganeh
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
; FILE REFERENCE: PI-0417 USA
; CURRENT APPLICATION NUMBER: US/10/287,218
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; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/11152
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/349,705
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/295,263
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/295,340
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/293,727
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/291,846
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/291,662
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/287,228
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/286,820
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/283,294
; PRIOR FILING DATE: 2001-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030198975A1 6937367CD1
US-10-287-218-9
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Query Match 85.8%; Score 609; DB 4; Length 710;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MERTAGKELALAPLDQWGEETEDGAVYSVLSRRQSRQSPAEQSGQAPSPANTFLH 60
Db 1 MERTAGKELALAPLDQWGEETEDGAVYSVLSRRQSRQSPAEQSGQAPSPANTFLH 60
Qy 61 YRTSKVRVLAARLERLVLGDEQDQSPFAFLATYRTFVPTACLLGFLLLPMPPP 120
Db 61 YRTSKVRVLAARLERLVLGDEQDQSPFAFLATYRTFVPTACLLGFLLLPMPPP 120
Qy 121 PPPGVEIKTAVQDLSPFNKRLRAVSVLGSWLDQHPQDFRDHPVHSDLGSVRTFLGWAAP 180
Db 121 PPPGVEIKTAVQDLSPFNKRLRAVSVLGSWLDQHPQDFRDHPVHSDLGSVRTFLGWAAP 180
Qy 181 GSAAQAKAEKLLDFLEAEAREQEEPPQVMTGPRVAQTSDDPSSEACAEBEGLMPOG 240
Db 181 GSAAQAKAEKLLDFLEAEAREQEEPPQVMTGPRVAQTSDDPSSEACAEBEGLMPOG 240
Qy 241 POLDFSDEVAEQTLIDLEFSKRVLYECLGSVMSQDRDRPAAAGASPTVATVAQFNT 300
Db 241 POLDFSDEVAEQTLIDLEFSKRVLYECLGSVMSQDRDRPAAAGASPTVATVAQFNT 300
Qy 301 VTGCVLGSVLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSRLAILSLAQSNPIYRLKR 360
Db 301 VTGCVLGSVLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSRLAILSLAQSNPIYRLKR 360
Qy 361 SWGAVSREPLSTFRKLSQIFSDNNHLSGREILFQEEATEGSEEDNTPGSLPSKPPGP 420
Db 361 SWGAVSREPLSTFRKLSQIFSDNNHLSGREILFQEEATEGSEEDNTPGSLPSKPPGP 420
Qy 421 VPYLGTFTLDVMDLTPALPDMLGDLINFEKRWKEWILLARIOQORRCQSYLSHPPI 480
Db 421 VPYLGTFTLDVMDLTPALPDMLGDLINFEKRWKEWILLARIOQORRCQSYLSHPPI 480
Qy 481 LAALHAQNLTEQSYRLSVIEPPAAACPSPPRRIRRLSLTKLSAKLAREKSSPSGS 540
Db 481 LAALHAQNLTEQSYRLSVIEPPAAACPSPPRRIRRLSLTKLSAKLAREKSSPSGS 540
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QY 541 PGDPSSPTSSVSPGSPSRSDAPAGSPGPGSTKPLSLDLSPRPFALPLG 600  
Db 541 PGDPSSPTSSVSPGSPSRSDAPAGSPGPGSTKPLSLDLSPRPFALPLG 600  
QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVPQWACD 660  
Db 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVPQWACD 660  
QY 661 YQLFQVLPGDRVLLIPDNANFYAMSPVAPRDFMLRRKEGTRNTLSVSPS 710  
Db 661 YQLFQVLPGDRVLLIPDNANFYAMSPVAPRDFMLRRKEGTRNTLSVSPS 710

## RESULT 5

US-10-474-291-9  
; Sequence 9, Application US/10474291  
; Publication No. US20040132043A1  
; GENERAL INFORMATION:  
; APPLICANT: AZIMZAI, Yalda; AU-YOUNG, Janice K.  
; APPLICANT: BATRA, Saijeev; BAUGHN, Mariah R.  
; APPLICANT: BECHA, Shanya D.; BOROMSKY, Mark L.  
; APPLICANT: BURFORD, Neil; DING, Li  
; APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.  
; APPLICANT: GANDHI, Aneena R.; GIETZEN, Kimberly J.  
; APPLICANT: GRIFFIN, Jennifer D.; HAFALIA, April J.A.  
; APPLICANT: HONCHELL, Cynthia D.; LAL, Preeti G.  
; APPLICANT: LEE, Soo Yeun; LU, Dzung Aina M.  
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi  
; APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.  
; APPLICANT: TANG, Y. Tom; CHAWLA, Narinder K.  
; APPLICANT: WANG, Yu-Mei E.; WARREN, Bridget A.  
; APPLICANT: XU, Yuming; YANG, Junming  
; APPLICANT: YAO, Monique G.; YUE, Henry  
; APPLICANT: ZEBARUADIAN, Yeganeh  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH  
; FILE REFERENCE: PI-0417 USN  
; CURRENT APPLICATION NUMBER: US/10/474,291  
; PRIOR FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: PCT/US02/11152  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: US 60/349,705  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: US 60/295,263  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/295,340  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/293,727  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/291,846  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/291,662  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: US 60/287,228  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/286,820  
; PRIOR FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: US 60/283,294  
; PRIOR FILING DATE: 2001-04-11  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PERL Program  
; SEQ ID NO 9  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 6937367CD1  
US-10-474-291-9

Query Match 85.8%; Score 609; DB 4; Length 710;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MERTAGKELALAPLDWGEETEDGAVYSVLSRQRORRSPAGSGSQAPSPANTFLH 60  
Db 1 MERTAGKELALAPLDWGEETEDGAVYSVLSRQRORRSPAGSGSQAPSPANTFLH 60  
QY 61 YRTSKVRLRAARLERLVGELVFGDREQDPSFMPAFATYRTFVPTACLLGFLLPMPPPP 120  
Db 61 YRTSKVRLRAARLERLVGELVFGDREQDPSFMPAFATYRTFVPTACLLGFLLPMPPPP 120  
QY 121 PPGVEIKKTAVQDLSFNKNLRAVSVGLSWLQOHQODFRDHPVHSDGLSVRTFLGWAAP 180  
Db 121 PPGVEIKKTAVQDLSFNKNLRAVSVGLSWLQOHQODFRDHPVHSDGLSVRTFLGWAAP 180  
QY 181 GSAEAOAKAEKLLDFLEAEAREOEERPPQVMTGPPRVAQTSDDPSSEACAEEEGLMQG 240  
Db 181 GSAEAOAKAEKLLDFLEAEAREOEERPPQVMTGPPRVAQTSDDPSSEACAEEEGLMQG 240  
QY 241 POLLDFSVDEVAEQTLTDLLEFYSKVLRYECLGSVMSQDRDPGAAGASPTVRATVAQNT 300  
Db 241 POLLDFSVDEVAEQTLTDLLEFYSKVLRYECLGSVMSQDRDPGAAGASPTVRATVAQNT 300  
QY 301 VTCGVLSVGLGAPGLAAPQRAQLEKWIRIAQRCRELNFESSRLAISALQSNIYRLKR 360  
Db 301 VTCGVLSVGLGAPGLAAPQRAQLEKWIRIAQRCRELNFESSRLAISALQSNIYRLKR 360  
QY 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEEDNTPGSLPSKPPPGP 420  
Db 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEEDNTPGSLPSKPPPGP 420  
QY 421 VPYLGTFDLTDLVMDLTALPDMLEGDLINFEKRRKEWEILLARIQOLQRRCSYTLSPHPI 480  
Db 421 VPYLGTFDLTDLVMDLTALPDMLEGDLINFEKRRKEWEILLARIQOLQRRCSYTLSPHPI 480  
QY 481 LAALHAQNLTEQSVRLSRVIEPPAASCPSSPRIIRRIISLTSLKLSAKLAREKSSSPSGS 540  
Db 481 LAALHAQNLTEQSVRLSRVIEPPAASCPSSPRIIRRIISLTSLKLSAKLAREKSSSPSGS 540  
QY 541 PGDPSSPTSSVSPGSPSRSDAPAGSPGPGSTKPLSLDLSPRPFALPLG 600  
Db 541 PGDPSSPTSSVSPGSPSRSDAPAGSPGPGSTKPLSLDLSPRPFALPLG 600  
QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVPQWACD 660  
Db 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVPQWACD 660  
QY 661 YQLFQVLPGDRVLLIPDNANFYAMSPVAPRDFMLRRKEGTRNTLSVSPS 710  
Db 661 YQLFQVLPGDRVLLIPDNANFYAMSPVAPRDFMLRRKEGTRNTLSVSPS 710

## RESULT 6

US-10-894-680A-3  
; Sequence 3, Application US/10894680A  
; Publication No. US20050176021A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: NGUYEN, Cung-Tuong  
; TITLE OF INVENTION: HUMAN RALGDS-LIKE PROTEIN 3  
; FILE REFERENCE: PB0176  
; CURRENT APPLICATION NUMBER: US/10/894,680A  
; CURRENT FILING DATE: 2004-07-19  
; PRIOR APPLICATION NUMBER: 10/060,990  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 09/864,761  
;; PRIOR FILING DATE: 2001-05-23  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 68  
;; SOFTWARE: Acmica Sequence Listing Engine  
;; SEQ ID NO 3  
;; LENGTH: 710  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-894-680A-3

Query Match 85.8%; Score 609; DB 5; Length 710;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MERTAGKELALAPLQDWGEETEDGAVYSVLSRRQESQRESPAEGGSGQAPSPANTFLH 60  
DB 1 MERTAGKELALAPLQDWGEETEDGAVYSVLSRRQESQRESPAEGGSGQAPSPANTFLH 60  
QY 61 YRTSKVRLRAARLERLVGELVFGDREODPSFMPAFATYRTFTACLLGFLPLPMPPP 120  
DB 61 YRTSKVRLRAARLERLVGELVFGDREODPSFMPAFATYRTFTACLLGFLPLPMPPP 120  
QY 121 PPPGVEIKTAVQDLSFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLSGVRTFLGWAAP 180  
DB 121 PPPGVEIKTAVQDLSFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLSGVRTFLGWAAP 180  
QY 181 GSAEAKAEKLLLEDFEAEAREOEPEEPQVMTGPRVAQTSDDPSSSEACAESEGLMPQG 240  
DB 181 GSAEAKAEKLLLEDFEAEAREOEPEEPQVMTGPRVAQTSDDPSSSEACAESEGLMPQG 240  
QY 241 POLDFFSDEVAEQLTLIDLELFSKVRLYECLGSVWSQDRPGAGASPTVRATVAQFNT 300  
DB 241 POLDFFSDEVAEQLTLIDLELFSKVRLYECLGSVWSQDRPGAGASPTVRATVAQFNT 300  
QY 301 VTGCVLGSVLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSLRALISALOSNPIYRLKR 360  
DB 301 VTGCVLGSVLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSLRALISALOSNPIYRLKR 360  
QY 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEEATEGSEEDNTPGSLPSKPPGP 420  
DB 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEEATEGSEEDNTPGSLPSKPPGP 420  
QY 421 VPYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWEILARIQOLQRRCSQYTLSPHPI 480  
DB 421 VPYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWEILARIQOLQRRCSQYTLSPHPI 480  
QY 481 LAALHAQNOLTEQSYRLSRVIEPPAASCPSPRIRRRISITKRLSAKLAREKSSSPGSGS 540  
DB 481 LAALHAQNOLTEQSYRLSRVIEPPAASCPSPRIRRRISITKRLSAKLAREKSSSPGSGS 540  
QY 541 PGDSSPTSSVSGSPSSPSRSDAPAGSPASPGQPGPSTKPLPLSLDLPSPRFPALPLG 600  
DB 541 PGDSSPTSSVSGSPSSPSRSDAPAGSPASPGQPGPSTKPLPLSLDLPSPRFPALPLG 600  
QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILITSDQKAPSVRRALQKHNVPQWACD 660  
DB 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILITSDQKAPSVRRALQKHNVPQWACD 660  
QY 661 YQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
DB 661 YQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710

RESULT 7  
US-09-808-701A-33  
; Sequence 33, Application US/09808701A

;; Publication No. US20020146757A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Tang, Y. Tom  
;; APPLICANT: Goodrich, Ryle  
;; APPLICANT: Asundi, Vinod  
;; APPLICANT: Drmanac, Radoje T.  
;; TITLE OF INVENTION: No. 6610536el Nucleic Acids and  
;; FILE REFERENCE: 790CIP2D  
;; CURRENT APPLICATION NUMBER: US/09/808,701A  
;; CURRENT FILING DATE: 2002-03-14  
;; PRIOR APPLICATION NUMBER: 09/649,167 ✓  
;; PRIOR FILING DATE: 2000-08-23  
;; PRIOR APPLICATION NUMBER: 09/540,217  
;; PRIOR FILING DATE: 2000-03-31  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: Pct\_Fl\_genes Version 2.0  
;; SEQ ID NO 33  
;; LENGTH: 715  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-808-701A-33

Query Match 68.6%; Score 487; DB 3; Length 715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 224 DSSEACAESEGLMPQGLDFFSDEVAEQLTLIDLELFSKVRLYECLGSVWSQDRPG 283  
DB 229 DSSEACAESEGLMPQGLDFFSDEVAEQLTLIDLELFSKVRLYECLGSVWSQDRPG 288  
QY 284 AAGASPTVRATVAQFNTVTCVLGSLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSL 343  
DB 289 AAGASPTVRATVAQFNTVTCVLGSLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSL 348  
QY 344 RAILSALOSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEEATEGSO 403  
DB 349 RAILSALOSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEEATEGSO 408  
QY 404 EEDNTPGSLPSKPPGPVPLGTFITDLVMDLTALPDMLEGLINFEKRRKEWEILARIQ 463  
DB 409 EEDNTPGSLPSKPPGPVPLGTFITDLVMDLTALPDMLEGLINFEKRRKEWEILARIQ 468  
QY 464 QLORRCSQYTLSPHPIALHAQNOLTEQSYRLSRVIEPPAASCPSPRIRRRISITK 523  
DB 469 QLORRCSQYTLSPHPIALHAQNOLTEQSYRLSRVIEPPAASCPSPRIRRRISITK 528  
QY 524 RLSAKLAREKSSSPGSGPGDPSPTSSVSGSPSSPSRSDAPAGSPASPGQPGPSTKL 583  
DB 529 RLSAKLAREKSSSPGSGPGDPSPTSSVSGSPSSPSRSDAPAGSPASPGQPGPSTKL 588  
QY 584 PLSIDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILITSDQKAPSV 643  
DB 589 PLSIDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILITSDQKAPSV 648  
QY 644 VRRALQKHNVPQWACDYQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 703  
DB 649 VRRALQKHNVPQWACDYQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 708  
QY 704 TLSVSPS 710  
DB 709 TLSVSPS 715

RESULT 8  
US-10-233-131-33  
; Sequence 33, Application US/10233131  
; Publication No. US20030096279A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Tang, Y. Tom  
;; APPLICANT: Zhou, Ping  
;; APPLICANT: Goodrich, Ryle  
;; APPLICANT: Asundi, Vinod

APPLICANT: Zhao, Qing A.  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Xue, Aidong J.  
APPLICANT: Ren, Feiyan  
APPLICANT: Wang, Dunrui  
APPLICANT: Chen, Rui-hong  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. US20030096279A1el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 790CIP2D DIVA  
CURRENT APPLICATION NUMBER: US/10/233,131  
CURRENT FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 09/808,701  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: pt\_FL\_genes Version 2.0  
SEQ ID NO 33  
LENGTH: 715  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-233-131-33

Query Match 68.6%; Score 487; DB 4; Length 715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	224	DSSACAEIEGLMPQGLLDPSVDEVAEQTLIDLELFSKVLRYECLGSVWSQRDPG	283
Db	229	DSSACAEIEGLMPQGLLDPSVDEVAEQTLIDLELFSKVLRYECLGSVWSQRDPG	288
Qy	284	AAGASPTVRATVAQNTVTCVGLSVGAPGLAAPQRAQRLKIRIAQRCRELNFSS	343
Db	289	AAGASPTVRATVAQNTVTCVGLSVGAPGLAAPQRAQRLKIRIAQRCRELNFSS	348
Qy	344	RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ	403
Db	349	RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ	408
Qy	404	EEDNTPGSLPKPPPGPVYLGFTLTDVMDLTALPDMLEGLDINFEKRRKEWEILARIQ	463
Db	409	EEDNTPGSLPKPPPGPVYLGFTLTDVMDLTALPDMLEGLDINFEKRRKEWEILARIQ	468
Qy	464	QLORRCQSYTLSPHPPIALAAHAQNLTQEQSYRLSRVIEPPAAASCPSSPRIIRRLSLTK	523
Db	469	QLORRCQSYTLSPHPPIALAAHAQNLTQEQSYRLSRVIEPPAAASCPSSPRIIRRLSLTK	528
Qy	524	RLSAKLAREKSSSPSGSPGDPSSPTSSVSPGSPSSPRSDAPAGSPASPGPGPSTKL	583
Db	529	RLSAKLAREKSSSPSGSPGDPSSPTSSVSPGSPSSPRSDAPAGSPASPGPGPSTKL	588
Qy	584	PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSDQKAPSV	643
Db	589	PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSDQKAPSV	648
Qy	644	VRRALQKHNVQPMWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN	703
Db	649	VRRALQKHNVQPMWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN	708
Qy	704	TLVSFSPS 710	
Db	709	TLVSFSPS 715	

## RESULT 9

US-10-240-145-85  
Sequence 85, Application US/10240145  
Publication No. US20030235883A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 21272-048  
CURRENT APPLICATION NUMBER: US/10/240,145  
CURRENT FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/668,680  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/695,618  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 09/728,711  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: NOT YET ASSIGNED  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: Custom  
SEQ ID NO 85  
LENGTH: 715  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-240-145-85

Query Match 68.6%; Score 487; DB 4; Length 715;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	224	DSSACAEIEGLMPQGLLDPSVDEVAEQTLIDLELFSKVLRYECLGSVWSQRDPG	283
Db	229	DSSACAEIEGLMPQGLLDPSVDEVAEQTLIDLELFSKVLRYECLGSVWSQRDPG	288
Qy	284	AAGASPTVRATVAQNTVTCVGLSVGAPGLAAPQRAQRLKIRIAQRCRELNFSS	343
Db	289	AAGASPTVRATVAQNTVTCVGLSVGAPGLAAPQRAQRLKIRIAQRCRELNFSS	348
Qy	344	RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ	403
Db	349	RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ	408
Qy	404	EEDNTPGSLPKPPPGPVYLGFTLTDVMDLTALPDMLEGLDINFEKRRKEWEILARIQ	463
Db	409	EEDNTPGSLPKPPPGPVYLGFTLTDVMDLTALPDMLEGLDINFEKRRKEWEILARIQ	468
Qy	464	QLORRCQSYTLSPHPPIALAAHAQNLTQEQSYRLSRVIEPPAAASCPSSPRIIRRLSLTK	523
Db	469	QLORRCQSYTLSPHPPIALAAHAQNLTQEQSYRLSRVIEPPAAASCPSSPRIIRRLSLTK	528
Qy	524	RLSAKLAREKSSSPSGSPGDPSSPTSSVSPGSPSSPRSDAPAGSPASPGPGPSTKL	583
Db	529	RLSAKLAREKSSSPSGSPGDPSSPTSSVSPGSPSSPRSDAPAGSPASPGPGPSTKL	588
Qy	584	PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSDQKAPSV	643
Db	589	PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSDQKAPSV	648
Qy	644	VRRALQKHNVQPMWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN	703
Db	649	VRRALQKHNVQPMWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN	708
Qy	704	TLVSFSPS 710	
Db	709	TLVSFSPS 715	

## RESULT 10

US-10-291-128-85  
Sequence 85, Application US/10291128  
Publication No. US20050202422A1  
GENERAL INFORMATION:  
APPLICANT: Nuvelo, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIPA

APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6610536el Nucleic Acids and  
FILE REFERENCE: 790CIP2D  
CURRENT APPLICATION NUMBER: US/09/808,701A  
CURRENT FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: pt\_FL\_genes Version 2.0  
SEQ ID NO 34  
LENGTH: 699  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-808-701A-34

Query Match 68.6%; Score 487; DB 5; Length 715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 DSSACAEHEGLMPQGLDQFVDEVAEQLTLDLELFKVKLYECLGVSQDRPQ 283  
Db 229 DSSACAEHEGLMPQGLDQFVDEVAEQLTLDLELFKVKLYECLGVSQDRPQ 288  
Qy 284 AAGASPTVRATVAQNTVTGCVLGSVGLGAPLAAPQRAQLEKWRIRIAQRCRELNFSSL 343  
Db 289 AAGASPTVRATVAQNTVTGCVLGSVGLGAPLAAPQRAQLEKWRIRIAQRCRELNFSSL 348  
Qy 344 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEBATEGSQ 403  
Db 349 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEBATEGSQ 408  
Qy 404 EEDNTPGSLPSKPPGPPVYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 463  
Db 409 EEDNTPGSLPSKPPGPPVYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 468  
Qy 464 QLORRCQSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAASCPSPPRIRRIISLTK 523  
Db 469 QLORRCQSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAASCPSPPRIRRIISLTK 528  
Qy 524 RLSAKLAREKSSSPGSGPDSPSTSSVSGSPSSPSRSDAPAGSPASPQPGPSTKL 583  
Db 529 RLSAKLAREKSSSPGSGPDSPSTSSVSGSPSSPSRSDAPAGSPASPQPGPSTKL 588  
Qy 584 PLSLDLPSRPFALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643  
Db 589 PLSLDLPSRPFALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648  
Qy 644 VRRALQKHNVPQWACDYQLFQVLPGRDVR 672  
Db 649 VRRALQKHNVPQWACDYQLFQVLPGRDVR 677

RESULT 11  
US-09-808-701A-34  
Sequence 34, Application US/09808701A  
Publication No. US20020146757A1  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Goodrich, Ryle  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Xue, Aidong J.  
APPLICANT: Ren, Feiyan  
APPLICANT: Wang, Dunrui  
APPLICANT: Chen, Rui-hong  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. US20030096279A1el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides

APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 790CIP2D  
CURRENT APPLICATION NUMBER: US/09/808,701A  
CURRENT FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: pt\_FL\_genes Version 2.0  
SEQ ID NO 34  
LENGTH: 699  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-808-701A-34

Query Match 63.2%; Score 449; DB 3; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 DSSACAEHEGLMPQGLDQFVDEVAEQLTLDLELFKVKLYECLGVSQDRPQ 283  
Db 229 DSSACAEHEGLMPQGLDQFVDEVAEQLTLDLELFKVKLYECLGVSQDRPQ 288  
Qy 284 AAGASPTVRATVAQNTVTGCVLGSVGLGAPLAAPQRAQLEKWRIRIAQRCRELNFSSL 343  
Db 289 AAGASPTVRATVAQNTVTGCVLGSVGLGAPLAAPQRAQLEKWRIRIAQRCRELNFSSL 348  
Qy 344 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEBATEGSQ 403  
Db 349 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEBATEGSQ 408  
Qy 404 EEDNTPGSLPSKPPGPPVYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 463  
Db 409 EEDNTPGSLPSKPPGPPVYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 468  
Qy 464 QLORRCQSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAASCPSPPRIRRIISLTK 523  
Db 469 QLORRCQSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAASCPSPPRIRRIISLTK 528  
Qy 524 RLSAKLAREKSSSPGSGPDSPSTSSVSGSPSSPSRSDAPAGSPASPQPGPSTKL 583  
Db 529 RLSAKLAREKSSSPGSGPDSPSTSSVSGSPSSPSRSDAPAGSPASPQPGPSTKL 588  
Qy 584 PLSLDLPSRPFALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643  
Db 589 PLSLDLPSRPFALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648  
Qy 644 VRRALQKHNVPQWACDYQLFQVLPGRDVR 672  
Db 649 VRRALQKHNVPQWACDYQLFQVLPGRDVR 677

RESULT 12  
US-10-233-131-34  
Sequence 34, Application US/10233131  
Publication No. US20030096279A1  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Goodrich, Ryle  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Xue, Aidong J.  
APPLICANT: Ren, Feiyan  
APPLICANT: Wang, Dunrui  
APPLICANT: Chen, Rui-hong  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. US20030096279A1el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 790CIP2D DIVA  
CURRENT APPLICATION NUMBER: US/10/233,131  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 09/808,701  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: pc\_FU\_genes Version 2.0  
SEQ ID NO 34  
LENGTH: 699  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-233-131-34

Query Match 63.2%; Score 449; DB 4; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	224	DSSEACAEEEGLMPQGLDPSVDEVAEQLTLIDLEFSKVRLYECLGVSWSQRDPG	283
Db	229	DSSEACAEEEGLMPQGLDPSVDEVAEQLTLIDLEFSKVRLYECLGVSWSQRDPG	288
Qy	284	AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAAPQRAQLEKWKIRIAQRCRELNFSS	343
Db	289	AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAAPQRAQLEKWKIRIAQRCRELNFSS	348
Qy	344	RAILSALQSNPIYRLKRWGAVSREPLSTFRKLQIFSDENNHLSSREILFOEBATEGSQ	403
Db	349	RAILSALQSNPIYRLKRWGAVSREPLSTFRKLQIFSDENNHLSSREILFOEBATEGSQ	408
Qy	404	EEDNTGSLPKPPGPPVYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWELIARIQ	463
Db	409	EEDNTGSLPKPPGPPVYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWELIARIQ	468
Qy	464	QLORRQCSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAASCSPSPRIRRLISLTK	523
Db	469	QLORRQCSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAASCSPSPRIRRLISLTK	528
Qy	524	RLSAKLAREKSSSPGSGDPSSPTSSVSPGSPSPSRDAPAGSPGPGPSTKL	583
Db	529	RLSAKLAREKSSSPGSGDPSSPTSSVSPGSPSPSRDAPAGSPGPGPSTKL	588
Qy	584	PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV	643
Db	589	PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV	648
Qy	644	VRRALQKHNVPQWACDYQLFQVLPGRV	672
Db	649	VRRALQKHNVPQWACDYQLFQVLPGRV	677

RESULT 13  
US-10-240-145-86  
Sequence 86, Application US/10240145  
Publication No. US20030235883A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 21272-048  
CURRENT APPLICATION NUMBER: US/10/240,145  
CURRENT FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/668,680  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/695,618  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 09/728,711

PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: NOT YET ASSIGNED  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: Custom  
SEQ ID NO 86  
LENGTH: 699  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-240-145-86

Query Match 63.2%; Score 449; DB 4; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	224	DSSEACAEEEGLMPQGLDPSVDEVAEQLTLIDLEFSKVRLYECLGVSWSQRDPG	283
Db	229	DSSEACAEEEGLMPQGLDPSVDEVAEQLTLIDLEFSKVRLYECLGVSWSQRDPG	288
Qy	284	AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAAPQRAQLEKWKIRIAQRCRELNFSS	343
Db	289	AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAAPQRAQLEKWKIRIAQRCRELNFSS	348
Qy	344	RAILSALQSNPIYRLKRWGAVSREPLSTFRKLQIFSDENNHLSSREILFOEBATEGSQ	403
Db	349	RAILSALQSNPIYRLKRWGAVSREPLSTFRKLQIFSDENNHLSSREILFOEBATEGSQ	408
Qy	404	EEDNTGSLPKPPGPPVYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWELIARIQ	463
Db	409	EEDNTGSLPKPPGPPVYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWELIARIQ	468
Qy	464	QLORRQCSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAASCSPSPRIRRLISLTK	523
Db	469	QLORRQCSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAASCSPSPRIRRLISLTK	528
Qy	524	RLSAKLAREKSSSPGSGDPSSPTSSVSPGSPSPSRDAPAGSPGPGPSTKL	583
Db	529	RLSAKLAREKSSSPGSGDPSSPTSSVSPGSPSPSRDAPAGSPGPGPSTKL	588
Qy	584	PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV	643
Db	589	PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV	648
Qy	644	VRRALQKHNVPQWACDYQLFQVLPGRV	672
Db	649	VRRALQKHNVPQWACDYQLFQVLPGRV	677

RESULT 14  
US-10-291-128-86  
Sequence 86, Application US/10291128  
Publication No. US20050202422A1  
GENERAL INFORMATION:  
APPLICANT: Nuvelo, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP4  
CURRENT APPLICATION NUMBER: US/10/291,128  
CURRENT FILING DATE: 2002-11-08  
CURRENT APPLICATION NUMBER: PCT/US01/10484  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/668,680  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/695,618  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 09/728,711  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: 09/808,701  
PRIOR FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 172



```
; SOFTWARE: Custom
; SEQ ID NO 86
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-128-86

Query Match      63.2%; Score 449; DB 5; Length 699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 DSSACAEELMPQGLDFFSDEVAEQLTLDLELFKSVRLYECLGWSVMSQDRPG 283
Db 229 DSSACAEELMPQGLDFFSDEVAEQLTLDLELFKSVRLYECLGWSVMSQDRPG 288
Qy 284 AAGASPTVRATVAQNTVTGCVLGVGAPGLAAPQRAORLEKWIRIAQRCRELNFSS 343
Db 289 AAGASPTVRATVAQNTVTGCVLGVGAPGLAAPQRAORLEKWIRIAQRCRELNFSS 348
Qy 344 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNNHLSREILFOEATEGSQ 403
Db 349 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNNHLSREILFOEATEGSQ 408
Qy 404 EEDNTPGSLPKPPPPVPYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 463
Db 409 EEDNTPGSLPKPPPPVPYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 468
Qy 464 QLQRCSQYTLSPHPPIALAAHAQNOLTEEQSYRLSRVIEPPAASCPSPIRRIRISLTK 523
Db 469 QLQRCSQYTLSPHPPIALAAHAQNOLTEEQSYRLSRVIEPPAASCPSPIRRIRISLTK 528
Qy 524 RLSAKLAREKSSSPGSDPSSPTSSVSGSPSSPRSRDAPAGSPASPQPGPSTKL 583
Db 529 RLSAKLAREKSSSPGSDPSSPTSSVSGSPSSPRSRDAPAGSPASPQPGPSTKL 588
Qy 584 PLSLDLSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643
Db 589 PLSLDLSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648
Qy 644 VRRALQKHNVQPWACDYQLFQVLPGRDV 672
Db 649 VRRALQKHNVQPWACDYQLFQVLPGRDV 677
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## RESULT 15

```
US-10-094-749-2959
; Sequence 2959, Application US/10094749
; Publication No. US20030219741A1
```

## GENERAL INFORMATION:

```
; APPLICANT: ISOGAI TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YORI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
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; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2959
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2959
```

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Query Match      61.3%; Score 435; DB 4; Length 464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 MPQGPQLDFFSDEVAEQLTLDLELFKSVRLYECLGWSVMSQDRPGAAGASPTVRATVA 296
Db 1 MPQGPQLDFFSDEVAEQLTLDLELFKSVRLYECLGWSVMSQDRPGAAGASPTVRATVA 60
Qy 297 QFNTVTGCVLGVGAPGLAAPQRAORLEKWIRIAQRCRELNFSSRLAISALQSNPIY 356
Db 61 QFNTVTGCVLGVGAPGLAAPQRAORLEKWIRIAQRCRELNFSSRLAISALQSNPIY 120
Qy 357 RLKRSWGAVSREPLSTFRKLSQIFSDENNNHLSREILFOEATEGSQEDNTPGSLPKP 416
Db 121 RLKRSWGAVSREPLSTFRKLSQIFSDENNNHLSREILFOEATEGSQEDNTPGSLPKP 180
Qy 417 PGPVPVYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQOLQRCSQYTLSP 476
Db 181 PGPVPVYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQOLQRCSQYTLSP 240
Qy 477 HPPIALAAHAQNOLTEEQSYRLSRVIEPPAASCPSPIRRIRISLTKRLSAKLAREKSSS 536
Db 241 HPPIALAAHAQNOLTEEQSYRLSRVIEPPAASCPSPIRRIRISLTKRLSAKLAREKSSS 300
Qy 537 PGSGPDPSPTSSVSGSPSSPRSRDAPAGSPASPQPGPSTKLPLSLDLSPRPFA 596
Db 301 PGSGPDPSPTSSVSGSPSSPRSRDAPAGSPASPQPGPSTKLPLSLDLSPRPFA 360
Qy 597 LPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVQ 656
Db 361 LPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVQ 420
Qy 657 WACDYQLFQVLPGRDV 671
Db 421 WACDYQLFQVLPGRDV 435
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Search completed: June 12, 2006, 12:20:19
Job time : 183 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2006, 11:55:55 ; Search time 202 Seconds  
(without alignments)  
1607.048 Million cell updates/sec

Title: US-10-694-438-2

Perfect score: 710

Sequence: 1 MERTAGKELAPLQDWGEE.....RDFMLRRKGRNTLSVSPS 710

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A Geneseq\_8.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*
- 9: geneseqp2005s.\*
- 10: geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	710	100.0	710	6	Abp57918 Human Ras
2	609	85.8	710	5	Aao15655 Human Ral
3	609	85.8	710	6	Abp58338 Human cel
4	487	68.6	715	4	Aau68555 Human nov
5	487	68.6	715	9	Aed08221 Mouse Ral
6	449	63.2	699	4	Aau68556 Human nov
7	449	63.2	699	9	Aed08222 Mouse Ral
8	435	61.3	464	6	Ada55391 Human pro
9	384	54.1	562	6	Abra11327 Human DIT
10	381	53.7	708	6	Abol15021 Human NOV
11	207	29.2	208	7	Adm05268 Human pro
12	207	29.2	208	9	Aec88198 Human CDN
13	48	6.8	70	4	Aam20233 Peptide #
14	48	6.8	70	4	Abb40566 Peptide #
15	48	6.8	70	4	Aam34328 Peptide #
16	48	6.8	70	4	Abd24860 Protein #
17	48	6.8	70	4	Aam74214 Human bon
18	48	6.8	70	4	Aam61424 Human bra
19	48	6.8	70	4	Abg56017 Human liv
20	48	6.8	70	5	Abg44171 Human pep
21	26	3.7	26	10	Aec38096 Human ser
22	20	2.8	20	5	Aao15656 Human Ral
23	17	2.4	677	4	Aau21657 Novel hum

#### ALIGNMENTS

##### RESULT 1

ABP57918  
ID ABP57918 standard; protein; 710 AA.

XX  
AC ABP57918;

XX  
DT 17-FEB-2003 (first entry)

XX  
DE Human Ras-like protein.

XX  
XX Human; Ras-like protein; antiinflammatory; cytostatic; gene therapy;

XX  
KW Human; inflammation; cancer.

XX  
OS Homo sapiens.

XX  
FN WO200283915-A2.

XX  
XX 24-OCT-2002.

XX  
PF 10-APR-2002; 2002WO-USO11111.

XX  
XX 10-APR-2001; 2001US-0282460P.

PR  
09-APR-2002; 2002US-00118328.

XX  
XX (PEKE ) PE CORP NY.

XX  
XX Yan C, Ketchum KA, Beasley EM;

XX  
XX WPI; 2003-093028/08.

XX  
XX N-PSDB; ABV99729, ABV99730.

XX  
XX New Ras-like protein polypeptides and polynucleotides are useful in diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, particularly cancer.

XX  
XX Claim 1; Fig 2; 98pp; English.

XX  
XX The invention relates to a novel human Ras-like protein. The protein of the invention has antiinflammatory and cytostatic activity. The polynucleotide encoding the Ras-like protein may have a use in gene therapy. The Ras-like protein polypeptides and polynucleotides are useful in diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, particularly cancer.

XX  
XX The present sequence represents the Ras-like protein of the invention.

XX  
XX Sequence 710 AA;

XX  
XX Sequence 710 AA;

Query Match		100.0%;	Score 710;	DB 6;	Length 710;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 710;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MERTAGKELALAPLDWGTEEDGAVYSLRRQRRSPAEFGSGSQAPSPFIANTFLH	60		
DB	1	MERTAGKELALAPLDWGTEEDGAVYSLRRQRRSPAEFGSGSQAPSPFIANTFLH	60		
QY	61	YRTSKVRLRAARLERLVGELVFGDREQDPSFMPAFATYRTFVPTACLLGFLLPMPPP	120		
DB	61	YRTSKVRLRAARLERLVGELVFGDREQDPSFMPAFATYRTFVPTACLLGFLLPMPPP	120		
QY	121	PPGVEIKKTAVQDLSFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLSGVSTELGWAAP	180		
DB	121	PPGVEIKKTAVQDLSFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLSGVSTELGWAAP	180		
QY	181	GSAEAKAEKLLDFLEEAEREQEPEPPQVWGTGPRVAQTSDDPSSEACAEEEGLMPQG	240		
DB	181	GSAEAKAEKLLDFLEEAEREQEPEPPQVWGTGPRVAQTSDDPSSEACAEEEGLMPQG	240		
QY	241	POLLDFSVDEVAEQLTLDLELFSKVLRYECLGSVMSQRDRGAGASPTVRATVAQNT	300		
DB	241	POLLDFSVDEVAEQLTLDLELFSKVLRYECLGSVMSQRDRGAGASPTVRATVAQNT	300		
QY	301	VTGCVLGSVLGAPGLAAPQRAQRLKIRIAQRCRELNFSSRAILSALQSNPIYRLKR	360		
DB	301	VTGCVLGSVLGAPGLAAPQRAQRLKIRIAQRCRELNFSSRAILSALQSNPIYRLKR	360		
QY	361	SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSGQEDNTPGSLPKPPGP	420		
DB	361	SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSGQEDNTPGSLPKPPGP	420		
QY	421	VPYLGTFLTDLVMDLTALPDMLGDLINFEKRRKEWEILARIQOLRRCSYTLSPHPPI	480		
DB	421	VPYLGTFLTDLVMDLTALPDMLGDLINFEKRRKEWEILARIQOLRRCSYTLSPHPPI	480		
QY	481	LAALHAQNLTEQSVRLSRVIEPPAASCPSFRIRRRISLTKRLSAKLAREKSSPSGS	540		
DB	481	LAALHAQNLTEQSVRLSRVIEPPAASCPSFRIRRRISLTKRLSAKLAREKSSPSGS	540		
QY	541	PGDPSPTSSVSGSPSPSRSDAPAGSPAPSPGQESTKPLSLDLPSRPPFALPLG	600		
DB	541	PGDPSPTSSVSGSPSPSRSDAPAGSPAPSPGQESTKPLSLDLPSRPPFALPLG	600		
QY	601	SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRALQKHNPQWACD	660		
DB	601	SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRALQKHNPQWACD	660		
QY	661	YQLFOVLPQDRVLLIPDNNANVFYAMSPVAPRDFMLRRKEGTRNTLSVSFS	710		
DB	661	YQLFOVLPQDRVLLIPDNNANVFYAMSPVAPRDFMLRRKEGTRNTLSVSFS	710		

RESULT 2

AAO15655

ID AAO15655 standard; protein; 710 AA.

XX AC AAO15655;

XX DT 31-OCT-2002 (first entry)

XX DE Human RalGDS-like protein 3 (RGL3).

XX KW Human; RalGDS-like protein 3; RGL3 associated disorder;

XX KW guanine nucleotide exchange factor; RGL3; gene therapy.

XX OS Homo sapiens.

XX FN EP1229132-A2.

XX PD 07-AUG-2002.

XX

PF	25-JAN-2002;	2002EP-00001159.
XX	30-JAN-2001;	2001WO-US0000563.
PR	30-JAN-2001;	2001WO-US0000564.
PR	30-JAN-2001;	2001WO-US0000565.
PR	30-JAN-2001;	2001WO-US0000566.
PR	30-JAN-2001;	2001WO-US0000567.
PR	30-JAN-2001;	2001WO-US0000568.
PR	30-JAN-2001;	2001WO-US0000569.
PR	30-JAN-2001;	2001WO-US0000570.
PR	23-MAY-2001;	2001US-00864761.
PR	28-SEP-2001;	2001US-0326105P.
XX	(AEOM-) AEOMICA INC.	
PA	Gu Y, Nguyen C;	
XX	WPI; 2002-620726/67.	
XX	N-PSDB; AAL44435.	
XX	Novel RalGDS-like protein 3, a guanine nucleotide exchange factor for	
PT	small GTPase Ral and downstream effector for both Rlt and Ras and nucleic	
PT	acid encoding it for diagnosing, treating disorders associated with RGL3.	
XX	Claim 13; Fig 3; 60pp; English.	
XX	The invention comprises the amino acid and coding sequence of the human	
CC	RalGDS-like protein 3 (RGL3). RGL3 is a guanine nucleotide exchange	
CC	factor for the small GTPase Ral and a downstream effector for both Rlt	
CC	and Ras. The RGL3 DNA and protein sequences of the invention are useful	
CC	for the diagnosis and treatment/prevention (e.g. gene therapy) of a	
CC	disorder associated with decreased or increased expression or activity of	
CC	human RGL3. The present amino acid sequence represents the human RGL3	
CC	protein	
XX	Sequence 710 AA;	
SQ	Query Match	85.8%; Score 609; DB 5; Length 710;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 709; Conservative	0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MERTAGKELALAPLDWGTEEDGAVYSLRRQRRSPAEFGSGSQAPSPFIANTFLH	60
DB	1	MERTAGKELALAPLDWGTEEDGAVYSLRRQRRSPAEFGSGSQAPSPFIANTFLH	60
QY	61	YRTSKVRLRAARLERLVGELVFGDREQDPSFMPAFATYRTFVPTACLLGFLLPMPPP	120
DB	61	YRTSKVRLRAARLERLVGELVFGDREQDPSFMPAFATYRTFVPTACLLGFLLPMPPP	120
QY	121	PPGVEIKKTAVQDLSFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLSGVSTELGWAAP	180
DB	121	PPGVEIKKTAVQDLSFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLSGVSTELGWAAP	180
QY	181	GSAEAKAEKLLDFLEEAEREQEPEPPQVWGTGPRVAQTSDDPSSEACAEEEGLMPQG	240
DB	181	GSAEAKAEKLLDFLEEAEREQEPEPPQVWGTGPRVAQTSDDPSSEACAEEEGLMPQG	240
QY	241	POLLDFSVDEVAEQLTLDLELFSKVLRYECLGSVMSQRDRGAGASPTVRATVAQNT	300
DB	241	POLLDFSVDEVAEQLTLDLELFSKVLRYECLGSVMSQRDRGAGASPTVRATVAQNT	300
QY	301	VTGCVLGSVLGAPGLAAPQRAQRLKIRIAQRCRELNFSSRAILSALQSNPIYRLKR	360
DB	301	VTGCVLGSVLGAPGLAAPQRAQRLKIRIAQRCRELNFSSRAILSALQSNPIYRLKR	360
QY	361	SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSGQEDNTPGSLPKPPGP	420
DB	361	SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSGQEDNTPGSLPKPPGP	420
QY	421	VPYLGTFLTDLVMDLTALPDMLGDLINFEKRRKEWEILARIQOLRRCSYTLSPHPPI	480
DB	421	VPYLGTFLTDLVMDLTALPDMLGDLINFEKRRKEWEILARIQOLRRCSYTLSPHPPI	480

QY 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSSPRIIRRRISLTKRLSAKLAREKSSPSGS 540  
 Db |||||  
 QY 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSSPRIIRRRISLTKRLSAKLAREKSSPSGS 540  
 Db |||||  
 QY 541 PGDPSSPTSSVSGSPSSPRSDAPAGSPGPGQSTKLPLSLDLPSPRPFPALPLG 600  
 Db |||||  
 QY 541 PGDPSSPTSSVSGSPSSPRSDAPAGSPGPGQSTKLPLSLDLPSPRPFPALPLG 600  
 Db |||||  
 QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSVVRALOKHNVPQWACD 660  
 Db |||||  
 QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSVVRALOKHNVPQWACD 660  
 Db |||||  
 QY 661 YQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
 Db |||||  
 QY 661 YQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
 Db |||||

RESULT 3  
 ABP58338  
 ID ABP58338 standard; protein; 710 AA.  
 AC ABP58338;  
 XX  
 XX  
 DT 07-APR-2003 (first entry)  
 XX  
 XX Human cell growth, differentiation and death protein CGDD-9.  
 XX  
 XX CGDD-9; cell growth; cell differentiation; cell death; human; cytostatic;  
 KW antidiabetic; hepatotropic; antiinflammatory; antipsoriatic;  
 KW antianemic; ophthalmologic; auditory; anticonvulsant;  
 KW cerebroprotective; neuroprotective; antiparkinsonian;  
 KW neuroleptic; tranquillizer; immunosuppressive; anti-HIV; antiallergic;  
 KW antiasthmatic; antithyroid; antidiabetic; dermatological; nephrotropic;  
 KW antirheumatic; antiarthritic; antitumor; antitubercular; antileishmanic;  
 KW antibacterial; fungicide; antiparasitic; protozoacide; antihelminthic;  
 KW antifertility; gynaecological; guanine nucleotide dissociation factor;  
 KW gene therapy.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200297032-A2.  
 PN  
 XX  
 XX 05-DEC-2002.  
 XX  
 XX 05-APR-2002; 2002WO-US011152.  
 XX  
 XX 06-APR-2001; 2001US-0282110P.  
 PR 11-APR-2001; 2001US-0283294P.  
 PR 26-APR-2001; 2001US-0286820P.  
 PR 27-APR-2001; 2001US-0287228P.  
 PR 16-MAY-2001; 2001US-0291662P.  
 PR 18-MAY-2001; 2001US-0291846P.  
 PR 25-MAY-2001; 2001US-0293727P.  
 PR 01-JUN-2001; 2001US-0295263P.  
 PR 01-JUN-2001; 2001US-0295340P.  
 PR 15-JAN-2002; 2002US-0349705P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA  
 XX Azimzai Y, Au-Young JK, Batra S, Baughn MR, Becha SD;  
 PI Borowski ML, Burford N, Ding L, Elliott VS, Emerling BM, Gandhi AR;  
 PI Gietzen KJ, Griffin JA, Hafalia AJA, Honchell CD, Lal PG, Lee SY;  
 PI Lu DAM, Arvizu CS, Ramkumar J, Reddy R, Sanjanwala MM, Tang YF;  
 PI Walia NK, Wang YE, Warren BA, Xu Y, Yang J, Yao MG, Yue H;  
 PI Zebardjian Y;  
 XX  
 XX WPI; 2003-140453/13.  
 DR N-PSDB; ABZ24697.  
 XX  
 XX Novel human proteins associated with cell growth, differentiation and  
 PT death, useful for treating, diagnosing or preventing cancer,  
 PT developmental, neurological, reproductive or autoimmune/inflammatory  
 PT disorders.

XX  
 PS  
 XX Claim 1; Page 196-197; 238pp; English.  
 CC The present sequence is the protein sequence of human CGDD-9, a novel  
 CC protein associated with cell growth, differentiation and death. The  
 CC sequence is predicted from Incyte clone 6937367CB1, which was isolated  
 CC from a fallopian tube tissue cDNA library. Structural features establish  
 CC the protein as being associated with cell growth, differentiation and  
 CC death, and further evidence suggests it to be a guanine nucleotide  
 CC dissociation factor. The invention is based on novel human CGDD-1 to -21  
 CC proteins (see ABP58330-50), the polynucleotides encoding them (see  
 CC ABZ24689-709), and to the use of these for the diagnosis, treatment or  
 CC prevention of cell proliferative disorders including cancer,  
 CC developmental disorders, neurological disorders, autoimmune disorders,  
 CC reproductive disorders, and disorders of the placenta, and in the  
 CC assessment of the effects of exogenous compounds on the activity and  
 CC expression of proteins and nucleic acids associated with cell growth,  
 CC differentiation and death  
 XX  
 XX Sequence 710 AA;  
 SQ  
 Query Match 85.8%; Score 609; DB 6; Length 710;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MERTAGKELALAPLQDGEETEDGAVYSVLRORRORRSPAEPPGSGQAPSPFIANTFLH 60  
 Db |||||  
 QY 1 MERTAGKELALAPLQDGEETEDGAVYSVLRORRORRSPAEPPGSGQAPSPFIANTFLH 60  
 Db |||||  
 QY 61 YRTSKVRVLAARLERLVGELVFGDREQDPSFMPAFATYRTFVTACILGFLLLPMPPP 120  
 Db |||||  
 QY 61 YRTSKVRVLAARLERLVGELVFGDREQDPSFMPAFATYRTFVTACILGFLLLPMPPP 120  
 Db |||||  
 QY 121 PPPGVEIKKTAVQLSFWNLRVAVSVLGSWLQHPQDFRDHPVHSDLGSVRTFLGWAAP 180  
 Db |||||  
 QY 121 PPPGVEIKKTAVQLSFWNLRVAVSVLGSWLQHPQDFRDHPVHSDLGSVRTFLGWAAP 180  
 Db |||||  
 QY 181 GSAAEQAKAEKLEDFLEAEAREEQEPPQVGTGPRVAQTSDDPDSEACAEEEGLMPOG 240  
 Db |||||  
 QY 181 GSAAEQAKAEKLEDFLEAEAREEQEPPQVGTGPRVAQTSDDPDSEACAEEEGLMPOG 240  
 Db |||||  
 QY 241 PLLDFFSVDEVAEQTLTDLDFSKVRLYECLGVSWSQDRPFGAGASPTVRATVAQNT 300  
 Db |||||  
 QY 241 PLLDFFSVDEVAEQTLTDLDFSKVRLYECLGVSWSQDRPFGAGASPTVRATVAQNT 300  
 Db |||||  
 QY 301 VTGCVLGSVLGAPGLAAPQRAQRLKWIIRIAQRCRELNFSSRLAILSALQSNPIYRLKR 360  
 Db |||||  
 QY 301 VTGCVLGSVLGAPGLAAPQRAQRLKWIIRIAQRCRELNFSSRLAILSALQSNPIYRLKR 360  
 Db |||||  
 QY 361 SWGAVSRPLSTFRKLQIFSDENNHLSSRIILFOEATEGSGQEDNTPGSLPSKPPPGP 420  
 Db |||||  
 QY 361 SWGAVSRPLSTFRKLQIFSDENNHLSSRIILFOEATEGSGQEDNTPGSLPSKPPPGP 420  
 Db |||||  
 QY 421 VPYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQQLQRRCSQSYTLSPHPPI 480  
 Db |||||  
 QY 421 VPYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQQLQRRCSQSYTLSPHPPI 480  
 Db |||||  
 QY 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSSPRIIRRRISLTKRLSAKLAREKSSPSGS 540  
 Db |||||  
 QY 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSSPRIIRRRISLTKRLSAKLAREKSSPSGS 540  
 Db |||||  
 QY 541 PGDPSSPTSSVSGSPSSPRSDAPAGSPGPGQSTKLPLSLDLPSPRPFPALPLG 600  
 Db |||||  
 QY 541 PGDPSSPTSSVSGSPSSPRSDAPAGSPGPGQSTKLPLSLDLPSPRPFPALPLG 600  
 Db |||||  
 QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSVVRALOKHNVPQWACD 660  
 Db |||||  
 QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSVVRALOKHNVPQWACD 660  
 Db |||||  
 QY 661 YQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
 Db |||||  
 QY 661 YQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
 Db |||||

## RESULT 4

AAU68555  
ID AAU68555 standard; protein; 715 AA.

XX AC AAU68555;

XX DT 16-JAN-2002 (first entry)

XX DE Human novel cytokine encoded by cDNA 790CIP2D\_16 #1.

XX KW Human; cytokine; cell proliferation; cell differentiation;  
KW antiinflammatory; stem cell growth factor; activin; inhibin; cancer;  
KW nervous system disease; neuropathy; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease; spinal cord disorder;  
KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;  
KW platelet disorder; thrombocytopaenia; stem cell disorder;  
KW aplastic anaemia; tissue regeneration; wound healing; ulcer;  
KW osteoporosis; osteoarthritis; bone degenerative disorder;  
KW periodontal disease; fibrosis; reperfusion; immune disorder; SCID;  
KW severe combined immunodeficiency; infection; autoimmune disorder;  
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;  
KW asthma; coagulation disorder; haemophilia; sepsis; nephritis;  
KW inflammatory bowel disease; food supplement; immunogen.

XX OS Homo sapiens.

XX PN WO200175093-A1.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US010484.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PR 22-SEP-2000; 2000US-00668680.

XX PR 23-OCT-2000; 2000US-00695618.

XX PR 30-NOV-2000; 2000US-00728711.

XX PR 14-MAR-2001; 2001US-00808701.

XX PA (HYSB-) HYSQ INC.

XX PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;  
PI Xu C, Yang Y, Zaho QA, Chen R, Wang D, Goodrich RW, Liu C;  
PI Dmanac RT;

XX DR WPI; 2001-626432/72.

XX DR N-PSDB; AAS59847.

XX PT New polypeptides and nucleic acids, useful for diagnosis, treatment of  
PT inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone  
PT degenerative disorders, cancer and promoting wound healing.

XX PS Claim 20; Page 277-278; 336pp; English.

XX CC The invention relates to isolated human polypeptides (which may be  
CC cytokines) and the polynucleotides encoding them. The protein is useful  
CC for identifying a compound which binds to it (e.g. modulators, agonists  
CC and antagonists). The polynucleotides are useful as an array for mismatch  
CC detection. The proteins and nucleic acids are useful as nutritional  
CC sources or supplements. The protein exhibits activity relating  
CC to cytokine, cell proliferation, cell differentiation, antiinflammatory,  
CC stem cell growth factor activity, immune stimulating or immune  
CC suppressing and activin or inhibin related activities. The proteins (and  
CC antibodies raised against them) and nucleic acids are therefore useful in  
CC the diagnosis and treatment of diseases and disorders such as cancer,  
CC central and peripheral nervous system diseases and neuropathies,  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular  
CC diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,  
CC thrombocytopaenia, stem cell disorders, aplastic anaemia, for  
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
CC growth, and in tissue repair, healing of burns, incisions, ulcers, for

CC treating osteoporosis, osteoarthritis, bone degenerative disorders, or  
CC periodontal disease, lung or liver fibrosis, reperfusion injury in  
CC various tissues, various immune deficiencies and disorders including  
CC severe combined immunodeficiency (SCID), bacterial or fungal infections,  
CC autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,  
CC diabetes mellitus, myasthenia gravis), allergic reactions and conditions,  
CC such as asthma or other respiratory problems, coagulation disorders,  
CC haemophilia), septic shock, sepsis, arthritis, nephritis and inflammatory  
CC bowel disease, viral infection and are useful in altering bodily  
CC characteristics. The present sequence represents a novel protein of the  
CC invention

XX SQ Sequence 715 AA;

Query Match 68.6%; Score 487; DB 4; Length 715;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSEACAESEEGMLPQGPQLLDFSVDEVAEQTLTDLFELFKVRLYECLGSVWSQDRPG 283

DB 229 DSSEACAESEEGMLPQGPQLLDFSVDEVAEQTLTDLFELFKVRLYECLGSVWSQDRPG 288

QY 284 AAGASPTVRATVAQNTVTGCVLGSVLGAPLAAPQRAQLEKWIIRIAQRCRELNFSSL 343

DB 289 AAGASPTVRATVAQNTVTGCVLGSVLGAPLAAPQRAQLEKWIIRIAQRCRELNFSSL 348

QY 344 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLQIFSDENNNHLSRREILFOEBATEGSQ 403

DB 349 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLQIFSDENNNHLSRREILFOEBATEGSQ 408

QY 404 EEDNTPGSLPSKPPPGVPYLGTFELTDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 463

DB 409 EEDNTPGSLPSKPPPGVPYLGTFELTDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 468

QY 464 QLORRCQSYTLSPHPPIALAHQNLTEQSYRLSRVIEPPAASCPSPPRIRRIISLTK 523

DB 469 QLORRCQSYTLSPHPPIALAHQNLTEQSYRLSRVIEPPAASCPSPPRIRRIISLTK 528

QY 524 RLSAKLAREKSSPSGSPGDPSSPTSSVSGSPSSPSRSDAPAGSPASPQGPSTKL 583

DB 529 RLSAKLAREKSSPSGSPGDPSSPTSSVSGSPSSPSRSDAPAGSPASPQGPSTKL 588

QY 584 FLSDLPLSPRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILITSDQKAPSV 643

DB 589 FLSDLPLSPRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILITSDQKAPSV 648

QY 644 VRRALQKHNVQPPWACDYQLFOVLPGDEVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 703

DB 649 VRRALQKHNVQPPWACDYQLFOVLPGDEVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 708

QY 704 TLSVSPS 710

DB 709 TLSVSPS 715

## RESULT 5

AE008221

ID AE008221 standard; protein; 715 AA.

XX AC AE008221;

XX DT 17-NOV-2005 (first entry)

DE Mouse RalGDS-like protein 3 SEQ ID NO: 85.

XX KW Immune stimulation; gene therapy; drug screening; transgenic animal;  
KW food; inflammation; antiinflammatory; autoimmune disease;  
KW immunosuppressive; immune disorder; autonomic nervous system disease;  
KW cns-gen.; neurological disease; central nervous system disease; leukemia;  
KW cytostatic; hematological disease; neoplasm; RalGDS-like protein 3.

XX OS Mus musculus.

XX

PN US2005202422-A1.  
 PD 15-SEP-2005.  
 PF 08-NOV-2002; 2002US-00291128.  
 XX 31-MAR-2000; 2000US-00540217.  
 PR 30-MAR-2001; 2001WO-US010484.  
 XX (TANG/) TANG Y T.  
 PA (LIUC/) LIU C.  
 PA (ASUN/) ASUNDI V.  
 PA (CHEN/) CHEN R.  
 PA (REN/) REN F.  
 PA (WANG/) WANG D.  
 PA (WANG/) WANG J.  
 PA (XUCC/) XU C.  
 PA (XUEA/) XUE A. J.  
 PA (YANG/) YANG Y.  
 PA (ZHAN/) ZHANG J.  
 PA (ZHAO/) ZHAO Q A.  
 PA (ZHOU/) ZHOU P.  
 PA (GOOD/) GOODRICH R W.  
 PA (DRWA/) DRWANAC R T.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ren F, Wang D, Wang J, Xu C;  
 PI Xue AJ, Yang Y, Zhang J, Zhao QA, Zhou P, Goodrich RW, Drmanac RT;  
 XX  
 DR WPI; 2005-618089/63.  
 DR N-PSDB; AED08178.  
 XX  
 PT New isolated polynucleotides, useful for treating, preventing, or  
 PT ameliorating, e.g. Alzheimer's disease, Parkinson's disease, Huntington's  
 PT disease, amyotrophic lateral sclerosis, or leukemia.  
 XX  
 PS Claim 20; SEQ ID NO 85; 60pp; English.  
 XX  
 CC The invention relates to polynucleotides and polypeptides capable of  
 CC inducing an immune response. The polynucleotides and proteins are useful  
 CC for treating, preventing or ameliorating a medical condition, e.g.  
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease,  
 CC amyotrophic lateral sclerosis, Shy-Drager syndrome or stroke. The  
 CC proteins can be used for treating leukemia, inflammatory disorders and  
 CC autoimmune disorders, e.g. multiple sclerosis, rheumatoid arthritis,  
 CC diabetes, myasthenia gravis or autoimmune inflammatory eye disease. They  
 CC can also be used as nutritional sources and supplements, e.g. as a carbon  
 CC source, nitrogen source or carbohydrate source. The sequences of the  
 CC invention are also useful in gene therapy, drug screening and in  
 CC production of transgenic animals. The present sequence is the mouse  
 CC RalGDS-like protein 3 of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docid=20050202422.  
 XX  
 SQ Sequence 715 AA;

Query Match 68.6%; Score 487; DB 9; Length 715;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSACAEEEGLMPQGGQLLDFSVDEVAEQLTDLLELFSKVLRYECLGSVWQSRDRPG 283  
 DB 229 DSSACAEEEGLMPQGGQLLDFSVDEVAEQLTDLLELFSKVLRYECLGSVWQSRDRPG 288  
 QY 284 AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAPQRAQLRKWIRIAQRCRELNFSSSL 343  
 DB 289 AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAPQRAQLRKWIRIAQRCRELNFSSSL 348  
 QY 344 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLQIFSDENNHLSSREILFQEBATEGSG 403  
 DB 349 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLQIFSDENNHLSSREILFQEBATEGSG 408  
 QY 404 EEDNTPGSLPKPPPGVPVYLTDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 463

DB 409 EEDNTPGSLPKPPPGVPVYLTDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 468  
 QY 464 QLQRRCSYTLSPHPPIALAHQONLTETOSYRLSRVIEPPAAACSPSPRIRRIISLTK 523  
 DB 469 QLQRRCSYTLSPHPPIALAHQONLTETOSYRLSRVIEPPAAACSPSPRIRRIISLTK 528  
 QY 524 RLSAKLAREKSSSPSGPDPSPPTSSVSPGSPSPSRSDAPAGSPASPGQPGPSTKL 583  
 DB 529 RLSAKLAREKSSSPSGPDPSPPTSSVSPGSPSPSRSDAPAGSPASPGQPGPSTKL 588  
 QY 584 PLSLDLSPRPFPALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSDQKAPSV 643  
 DB 589 PLSLDLSPRPFPALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSDQKAPSV 648  
 QY 644 VRRALQKHNVQPPWACDYQLFOVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 703  
 DB 649 VRRALQKHNVQPPWACDYQLFOVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 708  
 QY 704 TLSVSPS 710  
 DB 709 TLSVSPS 715

RESULT 6  
 AAU68556  
 ID AAU68556 standard; protein; 699 AA.  
 XX  
 AC AAU68556;  
 XX  
 DT 16-JAN-2002 (first entry)  
 DE Human novel cytokine encoded by cDNA 790CIP2D\_17 #1.  
 KW Human; cytokine; cell proliferation; cell differentiation;  
 KW antiinflammatory; stem cell growth factor; activin; inhibin; cancer;  
 KW nervous system disease; neuropathy; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; spinal cord disorder;  
 KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;  
 KW platelet disorder; thrombocytopaenia; stem cell disorder;  
 KW aplastic anaemia; tissue regeneration; wound healing; ulcer;  
 KW osteoporosis; osteoarthritis; bone degenerative disorder;  
 KW periodontal disease; fibrosis; reperfusion; immune disorder; SCID;  
 KW severe combined immunodeficiency; infection; autoimmune disorder;  
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;  
 KW asthma; coagulation disorder; haemophilia; sepsis; nephritis;  
 KW inflammatory bowel disease; food supplement; immunogen.

XX Homo sapiens.  
 XX OS  
 XX WO200175093-A1.  
 XX  
 PD 11-OCT-2001.  
 XX  
 XX 30-MAR-2001; 2001WO-US010484.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00643167.  
 PR 22-SEP-2000; 2000US-00668680.  
 PR 23-OCT-2000; 2000US-00695618.  
 PR 30-NOV-2000; 2000US-00728711.  
 PR 14-MAR-2001; 2001US-00808701.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;  
 PI Xu C, Yang Y, Zaho QA, Chen R, Wang D, Goodrich RW, Liu C;  
 PI Drmanac RT;  
 XX  
 DR WPI; 2001-626432/72.  
 DR N-PSDB; AAS59848.  
 XX  
 PT New polypeptides and nucleic acids, useful for diagnosis, treatment of

PT inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone  
XX degenerative disorders, cancer and promoting wound healing.  
PS Claim 20; Page 279-280; 336pp; English.

XX The invention relates to isolated human polypeptides (which may be  
XX cytokines) and the polynucleotides encoding them. The protein is useful  
XX for identifying a compound which binds to it (e.g. modulators, agonists  
XX and antagonists). The polynucleotides are useful as an array for mismatch  
XX detection. The proteins and nucleic acids are useful as nutritional  
XX sources or supplements. The protein exhibits activity relating  
XX to cytokine, cell proliferation, cell differentiation, antiinflammatory,  
XX stem cell growth factor activity, immune stimulating or immune  
XX suppressing and activin or inhibin related activities. The proteins (and  
XX antibodies raised against them) and nucleic acids are therefore useful in  
XX the diagnosis and treatment of diseases and disorders such as cancer,  
XX central and peripheral nervous system diseases and neuropathies,  
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
XX lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular  
XX diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,  
XX thrombocytopaenia, stem cell disorders, aplastic anaemia, for  
XX regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
XX growth, and in tissue repair, healing of burns, incisions, ulcers, for  
XX treating osteoporosis, osteoarthritis, bone degenerative disorders, or  
XX periodontal disease, lung or liver fibrosis, reperfusion injury in  
XX various tissues, various immune deficiencies and disorders including  
XX severe combined immunodeficiency (SCID), bacterial or fungal infections,  
XX autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,  
XX diabetes mellitus, myasthenia gravis), allergic reactions and conditions,  
XX such as asthma or other respiratory problems, coagulation disorders,  
XX haemophilia, septic shock, sepsis, arthritis, nephritis and inflammatory  
XX bowel disease, viral infection and are useful in altering bodily  
XX characteristics. The present sequence represents a novel protein of the  
XX invention

XX Sequence 699 AA;

Query Match 63.2%; Score 449; DB 4; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSEACAESEGLMPQGFLLDFSVDEVAQLTLDLELFSKVLRYECLGSVMSQDRPG 283  
Db 229 DSSEACAESEGLMPQGFLLDFSVDEVAQLTLDLELFSKVLRYECLGSVMSQDRPG 288  
QY 284 AAGASPTVATVAQNTVTCVLGSLVGLAPGLAQAQRAQLKRWIRIAQRCRELRFSSL 343  
Db 289 AAGASPTVATVAQNTVTCVLGSLVGLAPGLAQAQRAQLKRWIRIAQRCRELRFSSL 348  
QY 344 RAILSALQSNPIYRLKRSWAGVREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 403  
Db 349 RAILSALQSNPIYRLKRSWAGVREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 408  
QY 404 EEDNTGSLSPKPPGPPVPLGTFLTDLVMLDTPALDMLDGLINFEKRWELLARIQ 463  
Db 409 EEDNTGSLSPKPPGPPVPLGTFLTDLVMLDTPALDMLDGLINFEKRWELLARIQ 468  
QY 464 QLQRCOSYTLSPHPPTLAAHQAQNLTEQSVRLSRVIEPPPAACSPSPRIERRISLTK 523  
Db 469 QLQRCOSYTLSPHPPTLAAHQAQNLTEQSVRLSRVIEPPPAACSPSPRIERRISLTK 528  
QY 524 RLSAKLAREKSSPGSPGPPSSPTSSVSPGSPSPSRSDAPAGSPASPQGPSTKL 593  
Db 529 RLSAKLAREKSSPGSPGPPSSPTSSVSPGSPSPSRSDAPAGSPASPQGPSTKL 598  
QY 584 PLSLDLPSPPFPALPLGSPRIPPLPAQOSSEARVIRSIDNDHGNLYRSILLTSQDKAPSV 643  
Db 589 PLSLDLPSPPFPALPLGSPRIPPLPAQOSSEARVIRSIDNDHGNLYRSILLTSQDKAPSV 648  
QY 644 VRRALOKHNVPQWACDYQLFVLPGDRV 672  
Db 649 VRRALOKHNVPQWACDYQLFVLPGDRV 677

RESULT 7

AED08222  
ID AED08222 standard; protein; 699 AA.

XX AC AED08222;

XX 17-NOV-2005 (first entry)

XX Mouse RalGDS-like protein 3 SEQ ID NO: 86.

XX Immune stimulation; gene therapy; drug screening; transgenic animal;  
XX food; inflammation; antiinflammatory; autoimmune disease;  
XX immunosuppressive; immune disorder; autonomic nervous system disease;  
XX cns-gen.; neurological disease; central nervous system disease; leukemia;  
XX cytostatic; hematological disease; neoplasm; RalGDS-like protein 3.

OS Mus musculus.

XX US2005202422-A1.

XX 15-SEP-2005.

XX 08-NOV-2002; 2002US-00291128.

XX 31-MAR-2000; 2000US-00540217.

XX 30-MAR-2001; 2001WO-US010484.

XX (TANG/) TANG Y T.

XX (LIUC/) LIU C.

XX (ASUN/) ASUNDI V.

XX (CHEN/) CHEN R.

XX (REN/) REN F.

XX (WANG/) WANG D.

XX (WANG/) WANG J.

XX (XUE/) XUE A J.

XX (YANG/) YANG Y.

XX (ZHAN/) ZHANG J.

XX (ZHAO/) ZHAO Q A.

XX (ZHOU/) ZHOU P.

XX (GOOD/) GOODRICH R W.

XX (DRMA/) DRMANAC R T.

XX Tang YT, Liu C, Asundi V, Chen R, Ren F, Wang D, Wang J, Xu C;

XX Xue AJ, Yang Y, Zhang J, Zhao QA, Zhou P, Goodrich RW, Drmanac RT;

XX WPI; 2005-618089/63.

XX N-PSDB; AED08179.

XX New isolated polynucleotides, useful for treating, preventing, or

XX ameliorating, e.g. Alzheimer's disease, Parkinson's disease, Huntington's

XX disease, amyotrophic lateral sclerosis, or leukemia.

XX Claim 20; SEQ ID NO 86; 60pp; English.

XX The invention relates to polynucleotides and polypeptides capable of

XX inducing an immune response. The polynucleotides and proteins are useful

XX for treating, preventing or ameliorating a medical condition, e.g.

XX Alzheimer's disease, Parkinson's disease, Huntington's disease, The

XX amyotrophic lateral sclerosis, Shy-Drager syndrome or stroke. The

XX proteins can be used for treating leukemia, inflammatory disorders and

XX autoimmune disorders, e.g. multiple sclerosis, rheumatoid arthritis,

XX diabetes, myasthenia gravis or autoimmune inflammatory eye disease. They

XX can also be used as nutritional sources and supplements, e.g. as a carbon

XX source, nitrogen source or carbohydrate source. The sequences of the

XX invention are also useful in gene therapy, drug screening and in

XX production of transgenic animals. The present sequence is the mouse

XX RalGDS-like protein 3 of the invention. Note: The sequence data for this

XX patent did not form part of the invention. Note: The sequence data for this

XX in electronic format directly from USPTO at

XX seqdata.uspto.gov/sequence.html?DocID=20050202422.

XX

SQ Sequence 699 AA;  
 Query Match 63.2%; Score 449; DB 9; Length 699;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSACABEEBGLMPQGLDQFVDEVAEQLTLDLELFKVRLEYECLGVSQDRPQ 283  
 DB 229 DSSACABEEBGLMPQGLDQFVDEVAEQLTLDLELFKVRLEYECLGVSQDRPQ 288  
 QY 284 AAGASPTVRATVAQNTVTGCVLGSVGLGAPGLAAPQRAQLEKWIIRIAQRCRELNFSSSL 343  
 DB 289 AAGASPTVRATVAQNTVTGCVLGSVGLGAPGLAAPQRAQLEKWIIRIAQRCRELNFSSSL 348  
 QY 344 RAILSALQSNPIYRLKRSWGVSRPLSTFRKLQIFSDENNHLSSREILFQEEATEGSG 403  
 DB 349 RAILSALQSNPIYRLKRSWGVSRPLSTFRKLQIFSDENNHLSSREILFQEEATEGSG 408  
 QY 404 EEDNTPGSLPSKPPGPPVPLGTFTLDLVMLDTALPDMLEGLDINFEKRRKEWEILARIQ 463  
 DB 409 EEDNTPGSLPSKPPGPPVPLGTFTLDLVMLDTALPDMLEGLDINFEKRRKEWEILARIQ 468  
 QY 464 QLORCOSYTLSPHPPIALHAQNLTEEQSYLSRVIEPPAASCPSRRIRRIISLTK 523  
 DB 469 QLORCOSYTLSPHPPIALHAQNLTEEQSYLSRVIEPPAASCPSRRIRRIISLTK 528  
 QY 524 RLSAKLAREKSSSPGSGPPSSPTSSVSGSPSSPRSDAPAGSPGPGPSTKL 583  
 DB 529 RLSAKLAREKSSSPGSGPPSSPTSSVSGSPSSPRSDAPAGSPGPGPSTKL 588  
 QY 584 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643  
 DB 589 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648  
 QY 644 VRRALQKHNVQPPWACDYQLFQVLPQDRV 672  
 DB 649 VRRALQKHNVQPPWACDYQLFQVLPQDRV 677

RESULT 8  
 ADA55391 standard; protein; 464 AA.  
 AC ADA55391;  
 DT 20-NOV-2003 (first entry)  
 XX Human protein, SEQ ID 2959.  
 DE  
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;  
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;  
 KW inflammatory disease; osteoporosis; neurological disease.  
 OS Homo sapiens.  
 XX  
 PN EP1293569-A2.  
 XX  
 PD 19-MAR-2003.  
 XX  
 PF 21-MAR-2002; 2002EP-00006586.  
 XX  
 PR 14-SEP-2001; 2001JP-00328381.  
 PR 24-JAN-2002; 2002US-0350435P.  
 XX  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 XX  
 DR WPI; 2003-395539/38.  
 DR N-PSDB; ADA53752.

XX New polynucleotides encoding full-length polypeptides, e.g. secretory  
 PT and/or membrane proteins, useful for developing medicines for diseases in  
 PT which the gene is involved, or as target molecules for gene therapy.  
 XX  
 PS Claim 14; SEQ ID NO 2959; 205pp; English.  
 CC  
 CC The present invention relates to novel human secretory or membrane  
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-  
 CC ADA54071). The coding sequences are useful in the gene therapy of  
 CC diseases caused by abnormalities of the proteins, e.g. cancer,  
 CC inflammatory diseases, osteoporosis or neurological disease.  
 XX  
 SQ Sequence 464 AA;  
 Query Match 61.3%; Score 435; DB 6; Length 464;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 MPOGPQLDQFVDEVAEQLTLDLELFKVRLEYECLGVSQDRPQAGASPTVRATVA 296  
 DB 1 MPOGPQLDQFVDEVAEQLTLDLELFKVRLEYECLGVSQDRPQAGASPTVRATVA 60  
 QY 297 QFNTVTGCVLGSVGLGAPGLAAPQRAQLEKWIIRIAQRCRELNFSSRLAISALQSNPIY 356  
 DB 61 QFNTVTGCVLGSVGLGAPGLAAPQRAQLEKWIIRIAQRCRELNFSSRLAISALQSNPIY 120  
 QY 357 RLKRSWGVSRPLSTFRKLQIFSDENNHLSSREILFQEEATEGSGEEDNTPGSLPSKP 416  
 DB 121 RLKRSWGVSRPLSTFRKLQIFSDENNHLSSREILFQEEATEGSGEEDNTPGSLPSKP 180  
 QY 417 PPGPVYLGFTLDLVMLDTALPDMLEGLDINFEKRRKEWEILARIQLORCOSYTLSP 476  
 DB 181 PPGPVYLGFTLDLVMLDTALPDMLEGLDINFEKRRKEWEILARIQLORCOSYTLSP 240  
 QY 477 HPPILAAHAQNLTEEQSYLSRVIEPPAASCPSRRIRRIISLTKRLSAKLAREKSSS 536  
 DB 241 HPPILAAHAQNLTEEQSYLSRVIEPPAASCPSRRIRRIISLTKRLSAKLAREKSSS 300  
 QY 537 PGGSGDPSPSTSSVSGSPSSPRSDAPAGSPGPGPSTKLPLSLDLPSRPFPA 596  
 DB 301 PGGSGDPSPSTSSVSGSPSSPRSDAPAGSPGPGPSTKLPLSLDLPSRPFPA 360  
 QY 597 LPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVRRALQKHNVQPP 656  
 DB 361 LPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVRRALQKHNVQPP 420  
 QY 657 WACDYQLFQVLPQDR 671  
 DB 421 WACDYQLFQVLPQDR 435

RESULT 9  
 ABR41327  
 ID ABR41327 standard; protein; 562 AA.  
 XX  
 AC ABR41327;  
 XX  
 DT 02-JUN-2003 (first entry)  
 XX  
 DE Human DITHP intracellular signalling protein.  
 XX  
 KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
 KW cancer; cell proliferative disorder; autoimmune disorder;  
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
 KW neurological disorder; gastrointestinal disorder; transport disorder;  
 KW connective tissue disorder; drug screening; proteome analysis;  
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
 KW disease model; toxicological testing; transcript imaging;  
 KW intracellular signalling.  
 XX  
 OS Homo sapiens.  
 XX





16-FEB-2001; 2001US-0269530P.  
PR 15-MAR-2001; 2001US-0276405P.  
PR 16-MAR-2001; 2001US-0276399P.  
PR 16-MAR-2001; 2001US-0276703P.  
PR 23-MAR-2001; 2001US-0278199P.  
PR 28-MAR-2001; 2001US-0279274P.  
PR 30-MAR-2001; 2001US-0280238P.  
PR 02-APR-2001; 2001US-0280899P.  
PR 08-AUG-2001; 2001US-0310797P.  
PR 14-AUG-2001; 2001US-0312284P.  
PR 14-SEP-2001; 2001US-0322294P.  
PR 18-OCT-2001; 2001US-0330295P.  
PR 31-OCT-2001; 2001US-0335104P.  
PR 31-OCT-2001; 2001US-0335109P.  
PR 21-NOV-2001; 2001US-0332127P.  
PR 28-NOV-2001; 2001US-0331772P.  
XX  
FA (CURA-) CURAGEN CORP.  
XX  
XX Guo X, Fernandes E, Li L, Kekuda R, Liu Y, Leite M, Spytek KA;  
PI Ji W, Caeman SJ, Boldog FL, Patturajan M, Vernet CAM, Ballinger RA;  
PI Malyankar UM, Tchernev VT, Blalock AD, Gusev VI, Rastelli L;  
PI Mezes PD, Ellerman K, Heyes M, Herrmann JL, Shimkets RA, Ioime N;  
PI Pena CEA, Shenoy SG, Taupier RJ, Gerlach V, Gorman L;  
XX  
XX WPI; 2003-148650/14.  
DR N-PSDB; ACD20409.  
XX  
XX Novel NOVX polypeptide useful for identifying an agent that binds to the  
PT polypeptide, and for treating cardiomyopathy, atherosclerosis,  
PT hypertension, infertility, scleroderma, cirrhosis, and inflammatory bowel  
PT disease.  
XX  
PS Claim 1; Page 190; 566pp; English.  
XX  
XX The present invention relates to the isolation of novel human  
CC polypeptides referred to as NOVX (NOV1-NOV37), variants of these  
CC proteins, and the polynucleotide sequences encoding them. The NOVX  
CC proteins of the invention share homology to various types of protein  
CC families such as zinc finger-like proteins, enzymes, receptors, and  
CC lipoproteins. The sequences of the invention may be useful in the  
CC manufacture of a medicament for treating a syndrome associated with a  
CC human disease. For example they can be used to treat inflammatory  
CC disorders, demyelination disease, renal disorders, infections,  
CC cardiomyopathy, atherosclerosis, hypertension, stroke, pancreatitis, Von  
CC Hippel-Lindau, endometriosis, fertility, scleroderma, cirrhosis,  
CC inflammatory bowel disease, Crohn's disease, haemophilia, autoimmune  
CC diseases, allergies, graft versus host disease, Alzheimer's disease,  
CC arthritis, Parkinson's disease, Huntington's disease, obesity, diabetes,  
CC acne, hair growth/loss, asthma, schizophrenia, AIDS, pain,  
CC Glomerulonephritis, lupus erythematosus, and psoriasis. AB014984-AB015039  
CC represent the NOVX polypeptides of the invention. Note: SEQ ID Nos 113-  
CC 460 are known sequences used for homology purposes  
XX  
XX Sequence 708 AA;  
Query Match 53.7%; Score 381; DB 6; Length 708;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 213 GPRVQATSPDSSCAEEEGMLPQGPOLLDFSVDEVAEQTLTDLDFSKVRLYECL 272  
DB 211 GPRVQATSPDSSCAEEEGMLPQGPOLLDFSVDEVAEQTLTDLDFSKVRLYECL 270  
QY 273 GSVMSQDRPGAAGASTVTRATVAQNTVTGCVLGSVLGAPGLAAPQRAQRLKWRIRIAQ 332  
DB 271 GSVMSQDRPGAAGASTVTRATVAQNTVTGCVLGSVLGAPGLAAPQRAQRLKWRIRIAQ 330  
QY 333 RCRELNFSSRLAISLQNSPIYRLKRSNGAVSREPLSTFRKLSQIFSDENNHLSSREI 392  
DB 331 RCRELNFSSRLAISLQNSPIYRLKRSNGAVSREPLSTFRKLSQIFSDENNHLSSREI 390

393 LFOEEATEGSEQEEDNTPGSLPSPKPPGVPYLGFTLTDLVMDLTALPDMLEGLINFEKR 452  
QY  
DB 391 LFOEEATEGSEQEEDNTPGSLPSPKPPGVPYLGFTLTDLVMDLTALPDMLEGLINFEKR 450  
QY 453 RKEWEILARIQOLRRQCQSYTLSPHPPIAALHAQNOLTEEQSYRLSRVIEPPPAACSPSS 512  
DB 451 RKEWEILARIQOLRRQCQSYTLSPHPPIAALHAQNOLTEEQSYRLSRVIEPPPAACSPSS 510  
QY 513 PRIRRRISLTKRLSAKLAREKSSPSGSGDPPSSPTSSVSPGSPSPSRDRDAPAGSPPA 572  
DB 511 PRIRRRISLTKRLSAKLAREKSSPSGSGDPPSSPTSSVSPGSPSPSRDRDAPAGSPPA 570  
QY 573 SPGPGPSTKLPLSLDLPSR 593  
DB 571 SPGPGPSTKLPLSLDLPSR 591  
RESULT 11  
ADM05268  
ID ADM05268 standard; protein; 208 AA.  
XX  
AC ADM05268;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human protein of the invention SEQ ID NO:3953.  
XX  
XX human; gene therapy; diagnostic marker; pharmaceutical.  
XX  
OS Homo sapiens.  
XX  
PN EPI1347046-A1.  
XX  
PD 24-SEP-2003.  
XX  
PF 12-APR-2002; 2002EP-00008400.  
XX  
PR 22-MAR-2002; 2002JP-00137785.  
XX  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX  
XX WPI; 2003-723558/69.  
DR N-PSDB; ADM02825.  
XX  
XX New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.  
XX  
PS Claim 1; SEQ ID NO 3953; 305pp; English.  
XX  
XX The invention relates to a novel human polynucleotide and the encoded  
CC polypeptide. A polynucleotide of the invention ADM06202-ADM06773 is useful  
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
CC as a primer for synthesizing the polynucleotide or as a probe for  
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines  
CC for regulating their expression and activity, or as a target of gene  
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents a  
CC protein sequence of the invention.  
XX  
XX Sequence 208 AA;  
Query Match 29.2%; Score 207; DB 7; Length 208;  
Best Local Similarity 100.0%; Pred. No. 4.9e-188;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 237 MPQGPOLLDFSVDEVAEQTLTDLDFSKVRLYECLSGVMSQDRPGAAGASTVTRATVA 296

Db 1 MPQGPQLLDFSVDEVAEQTLTDLIDLELFSKVRLYECLGSVWSQDRPFGAAGASPTVRATVA 60  
 QY 297 QNTVTGCVLGSVLGAPGLAAPQRAQRLKWKIRIAQRCRELNFSSRLAILLSALQSNPIY 356  
 Db 61 QNTVTGCVLGSVLGAPGLAAPQRAQRLKWKIRIAQRCRELNFSSRLAILLSALQSNPIY 120  
 QY 357 RLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLPSKP 416  
 Db 121 RLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLPSKP 180  
 QY 417 PPGVPYILGTFLTDLVMLDTPDML 443  
 Db 181 PPGVPYILGTFLTDLVMLDTPDML 207

## RESULT 12

AEC88198  
 ID AEC88198 standard; protein; 208 AA.

AC AEC88198;

DT 01-DEC-2005 (first entry)

XX Human cDNA clone protein PROSTR20161950, SEQ ID 3953.

XX Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-Gen.;  
 KW Antulcer; Gene Therapy; Osteoporosis; cancer; inflammation; gastritis;  
 KW stomach ulcer; gastrointestinal ulcer.

XX Homo sapiens.

XX EPI580263-A1.

XX 28-SEP-2005.

XX 12-APR-2002; 2004EP-00027348.

XX 22-MAR-2002; 2002JP-00137785.

XX 12-APR-2002; 2002EP-00008400.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2005-667421/69.

XX N-PSDB; AEC85755.

XX New full-length cDNA sequences, useful for treating diseases, e.g.

XX osteoporosis, cancer, inflammation, gastritis, or gastroduodenal ulcer.

XX Example 3; SEQ ID NO 3953; 296pp; English.

XX The present invention relates to novel human cDNAs (AEC84246-AEC86688)  
 CC encoding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing  
 CC the functions of the proteins, and for developing medicines for diseases  
 CC e.g. osteoporosis, cancer, inflammation, gastritis, or gastroduodenal  
 CC ulcer. Note: The sequence data for this patent did not form part of the  
 CC printed specification but was obtained in electronic format directly from  
 CC EPO.

XX Sequence 208 AA;

Query Match 29.2%; Score 207; DB 9; Length 208;

Best Local Similarity 100.0%; Pred. No. 4.9e-188;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 MPQGPQLLDFSVDEVAEQTLTDLIDLELFSKVRLYECLGSVWSQDRPFGAAGASPTVRATVA 296

Db 1 MPQGPQLLDFSVDEVAEQTLTDLIDLELFSKVRLYECLGSVWSQDRPFGAAGASPTVRATVA 60

QY 297 QNTVTGCVLGSVLGAPGLAAPQRAQRLKWKIRIAQRCRELNFSSRLAILLSALQSNPIY 356

Db 61 QNTVTGCVLGSVLGAPGLAAPQRAQRLKWKIRIAQRCRELNFSSRLAILLSALQSNPIY 120  
 QY 357 RLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLPSKP 416  
 Db 121 RLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLPSKP 180  
 QY 417 PPGVPYILGTFLTDLVMLDTPDML 443  
 Db 181 PPGVPYILGTFLTDLVMLDTPDML 207

## RESULT 13

AAM20233

ID AAM20233 standard; protein; 70 AA.

XX AAM20233;

AC AAM20233;

DT 12-OCT-2001 (first entry)

XX Peptide #6667 encoded by probe for measuring cervical gene expression.

XX Probe; human; microarray; gene expression; cervical epithelial cell;

XX cervical cancer.

XX Homo sapiens.

XX WO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000670.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human cervical epithelial cells.

XX Claim 27; SEQ ID NO 25059; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes  
 CC (SENP; see AAI10068-AA128459). The present sequence is a peptide encoded  
 CC by one such probe. The SENPs are derived from human Hela cells. The SENPs  
 CC can be used to produce a single exon microarray, which can be used for  
 CC measuring human gene expression in a sample derived from human cervical  
 CC epithelial cells. By measuring gene expression, the probes are therefore  
 CC useful in grading and/or staging of diseases of the cervix, notably  
 CC cervical cancer. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 70 AA;

Query Match 6.8%; Score 48; DB 4; Length 70;

Best Local Similarity 100.0%; Pred. No. 4.8e-37;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 HSDLSGVRITFLGWAAPGSAEAKKLEDFLEAREQEPEPQVWT 212

Db 23 HSDLSGVRITFLGWAAPGSAEAKKLEDFLEAREQEPEPQVWT 70

```

RESULT 14
ABB40566
ID ABB40566 standard; peptide; 70 AA.
XX AC
XX ABB40566;
XX DT
XX 04-FEB-2002 (first entry)
XX DE Peptide #8072 encoded by human foetal liver single exon probe.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PFPI; 2001-483447/52.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human fetal liver.
XX PS Claim 27; SEQ ID NO 33201; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
XX CC displaying gene expression in samples derived from human fetal liver. The
XX CC present invention is a peptide encoded by a single exon nucleic acid probe
XX CC of the invention. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 70 AA;
XX Query Match 6.8%; Score 48; DB 4; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-37;
XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 165 HSDLGSVRTFLGWAAPGSAQAQAKLLEDFLEAEAEQEEPPQVWT 212
XX Db 23 HSDLGSVRTFLGWAAPGSAQAQAKLLEDFLEAEAEQEEPPQVWT 70
XX
RESULT 15
AAM34328
ID AAM34328 standard; protein; 70 AA.
XX AC
XX AAM34328;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #8365 encoded by probe for measuring placental gene expression.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.

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OS Homo sapiens.
XX WO200157272-A2.
XX PN
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PFPI; 2001-488897/53.
XX DR
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human placenta.
XX PS Claim 27; SEQ ID NO 34597; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AAI31315-RAI57546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders
XX SQ Sequence 70 AA;
XX Query Match 6.8%; Score 48; DB 4; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-37;
XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 165 HSDLGSVRTFLGWAAPGSAQAQAKLLEDFLEAEAEQEEPPQVWT 212
XX Db 23 HSDLGSVRTFLGWAAPGSAQAQAKLLEDFLEAEAEQEEPPQVWT 70
XX
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Job time : 206 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2006, 12:04:54 ; Search time 52 Seconds  
(without alignments)  
1195.130 Million cell updates/sec

Title: US-10-694-438-2

Perfect score: 710

Sequence: 1 MERTAGKELALAPLDQWGE.....RDFMLRKSGTNTLSVSPS 710

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 649417

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pdp:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pdp:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB.pdp:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS COMB.pdp:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pdp:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	710	100.0	710	2	US-10-118-328-2	Sequence 2, Appli
2	487	68.6	715	2	US-09-808-701A-33	Sequence 33, Appli
3	449	63.2	699	2	US-09-808-701A-34	Sequence 34, Appli
4	435	61.3	464	2	US-10-094-749-2959	Sequence 2959, Ap
5	47	6.6	709	2	US-10-118-328-4	Sequence 4, Appli
6	17	2.4	852	1	US-08-408-519-5	Sequence 5, Appli
7	17	2.4	852	5	PCT-US95-03552-5	Sequence 5, Appli
8	11	1.5	378	2	US-09-949-016-8733	Sequence 8733, Ap
9	11	1.5	725	2	US-10-118-328-5	Sequence 5, Appli
10	11	1.5	768	1	US-08-408-519-2	Sequence 2, Appli
11	11	1.5	768	5	PCT-US95-03552-2	Sequence 2, Appli
12	10	1.4	313	2	US-09-270-767-31859	Sequence 31859, A
13	10	1.4	313	2	US-09-270-767-47076	Sequence 47076, A
14	9	1.3	122	1	US-08-820-170A-1	Sequence 1, Appli
15	9	1.3	122	2	US-09-055-699-1	Sequence 1, Appli
16	9	1.3	122	2	US-09-273-565-1	Sequence 1, Appli
17	9	1.3	122	2	US-09-565-538-1	Sequence 1, Appli
18	9	1.3	122	2	US-09-661-468-1	Sequence 1, Appli
19	9	1.3	122	2	US-09-976-165-1	Sequence 1, Appli
20	9	1.3	420	2	US-09-902-540-12464	Sequence 12464, A
21	9	1.3	502	2	US-09-833-577A-14	Sequence 14, Appli
22	9	1.3	782	2	US-09-949-016-11571	Sequence 11571, A
23	8	1.1	26	1	US-07-942-245-391	Sequence 391, App
24	8	1.1	26	1	US-07-942-245-398	Sequence 398, App
25	8	1.1	65	1	US-07-808-457-7	Sequence 7, Appli
26	8	1.1	65	5	PCT-US92-10178-7	Sequence 7, Appli

27 8 1.1 77 2 US-09-621-976-4540 Sequence 4540, Ap  
28 8 1.1 91 1 US-07-808-457-11 Sequence 11, Appl  
29 8 1.1 91 5 PCT-US92-10178-11 Sequence 11, Appl  
30 8 1.1 139 1 US-07-808-457-13 Sequence 13, Appl  
31 8 1.1 139 5 PCT-US92-10178-13 Sequence 13, Appl  
32 8 1.1 149 1 US-07-808-457-15 Sequence 15, Appl  
33 8 1.1 149 2 US-09-621-976-5675 Sequence 5675, Ap  
34 8 1.1 149 5 PCT-US92-10178-15 Sequence 15, Appl  
35 8 1.1 150 1 US-07-808-457-17 Sequence 17, Appl  
36 8 1.1 150 5 PCT-US92-10178-17 Sequence 17, Appl  
37 8 1.1 155 2 US-09-252-991A-17954 Sequence 17954, A  
38 8 1.1 161 2 US-09-252-991A-27639 Sequence 27639, A  
39 8 1.1 164 1 US-07-808-457-19 Sequence 19, Appl  
40 8 1.1 164 5 PCT-US92-10178-19 Sequence 19, Appl  
41 8 1.1 197 2 US-09-252-991A-26537 Sequence 26537, A  
42 8 1.1 200 1 US-08-170-596-15 Sequence 15, Appl  
43 8 1.1 214 2 US-09-252-991A-24236 Sequence 24236, A  
44 8 1.1 240 7 5204445-2 Patent No. 5204445  
45 8 1.1 266 1 US-07-808-457-3 Sequence 3, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-118-328-2  
; Sequence 2, Application US/10118328  
; Patent No. 6773904  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE  
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL001220  
; CURRENT APPLICATION NUMBER: US/10/118,328  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/282,460  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-118-328-2

Query Match 100.0%; Score 710; DB 2; Length 710;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 710; Conservative, 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MERTAGKELALAPLDQWGEETEDGAVYSVLSRQRORRSPAEQGGSOAPSPIANTFLH 60  
DB 1 MERTAGKELALAPLDQWGEETEDGAVYSVLSRQRORRSPAEQGGSOAPSPIANTFLH 60  
QY 61 YRTSKVRVLAARLERLVGELVFGDREDDPSFMPAFIATYRTFTVFTACLLGFLPPMPP 120  
DB 61 YRTSKVRVLAARLERLVGELVFGDREDDPSFMPAFIATYRTFTVFTACLLGFLPPMPP 120  
QY 121 PPPVEIKTKTAVQDLSFNKNLRVAVVLSGLWQHPDQDFRDPVHSDLSGVRFLGWAAP 180  
DB 121 PPPVEIKTKTAVQDLSFNKNLRVAVVLSGLWQHPDQDFRDPVHSDLSGVRFLGWAAP 180  
QY 181 GSAEAKAEKLLDFLEAEAREQEEPPQVMTGPPRVAQTSDPDSSACAESEGLMPOG 240  
DB 181 GSAEAKAEKLLDFLEAEAREQEEPPQVMTGPPRVAQTSDPDSSACAESEGLMPOG 240  
QY 241 POLLDFSVDEVAEQTLTLDLELFSKVLRYECLGSVWSQDRPGAGASPTVRATVAQNT 300  
DB 241 POLLDFSVDEVAEQTLTLDLELFSKVLRYECLGSVWSQDRPGAGASPTVRATVAQNT 300  
QY 301 VTGCVLGSVLGAPCLAAPQRAQRLKWKIRTAQRCRELNFSSLRPAILSALOSNPIYLRK 360  
DB 301 VTGCVLGSVLGAPCLAAPQRAQRLKWKIRTAQRCRELNFSSLRPAILSALOSNPIYLRK 360

QY 361 SWGAVSREPLSTFRKLSQIFSDNNHLSREILFOEEATEGSQBEDNTPGSLPKPPGP 420  
DB 361 SWGAVSREPLSTFRKLSQIFSDNNHLSREILFOEEATEGSQBEDNTPGSLPKPPGP 420  
QY 421 VPIGLTFTLDVMDLTALPDMLEGLINFEKRWKWEILARIQLOQRCCQYITLSPPPI 480  
DB 421 VPIGLTFTLDVMDLTALPDMLEGLINFEKRWKWEILARIQLOQRCCQYITLSPPPI 480  
QY 481 LAALHAQNOLTEOSYRLSRVIEPPAASCPSRRIRISLTSLTKLSAKLAREKSSPSGS 540  
DB 481 LAALHAQNOLTEOSYRLSRVIEPPAASCPSRRIRISLTSLTKLSAKLAREKSSPSGS 540  
QY 541 PGDPSSPTSSVSPGSPSPSRDAPAGSPASPGQPGSTKLPLSLDLPSRPFALPLG 600  
DB 541 PGDPSSPTSSVSPGSPSPSRDAPAGSPASPGQPGSTKLPLSLDLPSRPFALPLG 600  
QY 601 SPRPLPAQOSSEARVIRVSDNDHGNLYRSILTSQDKAPSVRRALQKHNVQPWACD 660  
DB 601 SPRPLPAQOSSEARVIRVSDNDHGNLYRSILTSQDKAPSVRRALQKHNVQPWACD 660  
QY 661 YOLFQVLPGRVLLIPDNANFYAMSPVAPRDFMLRRKGTNTLSVSPS 710  
DB 661 YOLFQVLPGRVLLIPDNANFYAMSPVAPRDFMLRRKGTNTLSVSPS 710

## RESULT 2

US-09-808-701A-33  
; Sequence 33, Application US/09808701A  
; Patent No. 6610536  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Dmanac, Radoje T.  
; TITLE OF INVENTION: No. 6610536el Nucleic Acids and  
; FILE REFERENCE: 790CIP2D  
; CURRENT APPLICATION NUMBER: US/09/808,701A  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 33  
; LENGTH: 715  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-808-701A-33

Query Match 68.6%; Score 487; DB 2; Length 715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSEACAEEEGLMPQGPOLLDFSVDEVAEQTLTDLLELFSKRVLYECLGSVMSQDRPG 293  
DB 229 DSSEACAEEEGLMPQGPOLLDFSVDEVAEQTLTDLLELFSKRVLYECLGSVMSQDRPG 288  
QY 284 AAGASPTVRATVAQNTVTGCVLGSVLGAPLAAPQRAQLEKWKIRIAQRCRELNFSSL 343  
DB 289 AAGASPTVRATVAQNTVTGCVLGSVLGAPLAAPQRAQLEKWKIRIAQRCRELNFSSL 348  
QY 344 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDNNHLSREILFOEEATEGSQ 403  
DB 349 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDNNHLSREILFOEEATEGSQ 408  
QY 404 EEDNTPGSLPKPPGPVPYLGFTLTDVMDLTALPDMLEGLINFEKRWKWEILARIQ 463  
DB 409 EEDNTPGSLPKPPGPVPYLGFTLTDVMDLTALPDMLEGLINFEKRWKWEILARIQ 468  
QY 464 QLQRRCCQSYTLSPHPPIAALHAQNOLTEOSYRLSRVIEPPAASCPSRRIRISLTSLTK 523

DB 469 QLQRRCCQSYTLSPHPPIAALHAQNOLTEOSYRLSRVIEPPAASCPSRRIRISLTSLTK 528  
QY 524 RLSAKLAREKSSPSGSPGDPSPSTSSVSPGSPSRDAPAGSPASPGQPGSTKL 583  
DB 529 RLSAKLAREKSSPSGSPGDPSPSTSSVSPGSPSRDAPAGSPASPGQPGSTKL 588  
QY 584 PLSLDLPSRPFALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILTSQDKAPSV 643  
DB 589 PLSLDLPSRPFALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILTSQDKAPSV 648  
QY 644 VRRALQKHNVQPWACDYOLFQVLPGRVLLIPDNANFYAMSPVAPRDFMLRRKGTNRN 703  
DB 649 VRRALQKHNVQPWACDYOLFQVLPGRVLLIPDNANFYAMSPVAPRDFMLRRKGTNRN 708  
QY 704 TLSVSPS 710  
DB 709 TLSVSPS 715

## RESULT 3

US-09-808-701A-34  
; Sequence 34, Application US/09808701A  
; Patent No. 6610536  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Dmanac, Radoje T.  
; TITLE OF INVENTION: No. 6610536el Nucleic Acids and  
; FILE REFERENCE: 790CIP2D  
; CURRENT APPLICATION NUMBER: US/09/808,701A  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 34  
; LENGTH: 699  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-808-701A-34

Query Match 63.2%; Score 449; DB 2; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSEACAEEEGLMPQGPOLLDFSVDEVAEQTLTDLLELFSKRVLYECLGSVMSQDRPG 293  
DB 229 DSSEACAEEEGLMPQGPOLLDFSVDEVAEQTLTDLLELFSKRVLYECLGSVMSQDRPG 288  
QY 284 AAGASPTVRATVAQNTVTGCVLGSVLGAPLAAPQRAQLEKWKIRIAQRCRELNFSSL 343  
DB 289 AAGASPTVRATVAQNTVTGCVLGSVLGAPLAAPQRAQLEKWKIRIAQRCRELNFSSL 348  
QY 344 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDNNHLSREILFOEEATEGSQ 403  
DB 349 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDNNHLSREILFOEEATEGSQ 408  
QY 404 EEDNTPGSLPKPPGPVPYLGFTLTDVMDLTALPDMLEGLINFEKRWKWEILARIQ 463  
DB 409 EEDNTPGSLPKPPGPVPYLGFTLTDVMDLTALPDMLEGLINFEKRWKWEILARIQ 468  
QY 464 QLQRRCCQSYTLSPHPPIAALHAQNOLTEOSYRLSRVIEPPAASCPSRRIRISLTSLTK 523  
DB 469 QLQRRCCQSYTLSPHPPIAALHAQNOLTEOSYRLSRVIEPPAASCPSRRIRISLTSLTK 528  
QY 524 RLSAKLAREKSSPSGSPGDPSPSTSSVSPGSPSRDAPAGSPASPGQPGSTKL 583  
DB 529 RLSAKLAREKSSPSGSPGDPSPSTSSVSPGSPSRDAPAGSPASPGQPGSTKL 588

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QY 584 PLSLDLSPRPFPALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643
Db 589 PLSLDLSPRPFPALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648
QY 644 VRRALQKHNVQPWACDYQQLFQVLPGRV 672
Db 649 VRRALQKHNVQPWACDYQQLFQVLPGRV 677

RESULT 4
US-10-094-749-2959
; Sequence 2959, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2959
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2959

Query Match 61.3%; Score 435; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 MPQGPOLLDFSVDEVAEQTLIDLEFSKVRVYECGLSVMSQDRPFGAAGASPTVRATVA 296
Db 1 MPQGPOLLDFSVDEVAEQTLIDLEFSKVRVYECGLSVMSQDRPFGAAGASPTVRATVA 60
QY 297 QFNVTGCVLGSVGLGAPGAAPORAORLEKWIPIAORCRELNFSSRLSALQSNPIY 356
Db 61 QFNVTGCVLGSVGLGAPGAAPORAORLEKWIPIAORCRELNFSSRLSALQSNPIY 120
QY 357 RLKRSWGAVSREPLSTFRKLQSFSDNNHLSREILFOEATEGSOEDNTPGSLPSKP 416
Db 121 RLKRSWGAVSREPLSTFRKLQSFSDNNHLSREILFOEATEGSOEDNTPGSLPSKP 180
QY 417 PFGPVPYLTGFTLDVMDLTALPDMLEGLINFEXKREKWEILARIQQLQRCQSYTLSP 476
Db 181 PFGPVPYLTGFTLDVMDLTALPDMLEGLINFEXKREKWEILARIQQLQRCQSYTLSP 240
QY 477 HPPILAAHQNLTEQSYRISRVIEPPAASCPSFRIRRRISLTKRLSAKLAREKSSS 536
Db 241 HPPILAAHQNLTEQSYRISRVIEPPAASCPSFRIRRRISLTKRLSAKLAREKSSS 300
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QY 537 PSGPSGDPSPSTSSVSPGSPSRSDAPAGSPAPGPGQPGSTKPLSLDLPLSPRPFA 596
Db 301 PSGPSGDPSPSTSSVSPGSPSRSDAPAGSPAPGPGQPGSTKPLSLDLPLSPRPFA 360
QY 597 LPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVQP 656
Db 361 LPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVQP 420
QY 657 WACDYQLFQVLPGR 671
Db 421 WACDYQLFQVLPGR 435

RESULT 5
US-10-118-328-4
; Sequence 4, Application US/10118328
; Patent No. 6773904
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001220
; CURRENT APPLICATION NUMBER: US/10/118,328
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/282,460
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 709
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-118-328-4

Query Match 6.6%; Score 47; DB 2; Length 709;
Best Local Similarity 100.0%; Pred. No. 6.1e-35;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 325 EKWIRIAQRCRELNFSSRLSALQSNPIYRLKRSWGAVSREPLS 371
Db 326 EKWIRIAQRCRELNFSSRLSALQSNPIYRLKRSWGAVSREPLS 372

RESULT 6
US-08-408-519-5
; Sequence 5, Application US/08408519
; Patent No. 5955354
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Demo Susan
; TITLE OF INVENTION: A No. 5955354el ras p21-Interacting Protein and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,519
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
```

REFERENCE/DOCKET NUMBER: 02307K-56800  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 852 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-408-519-5

Query Match 2.4%; Score 17; DB 1; Length 852;  
Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 VPYLGTFLLDVLMLDTA 437  
|||||  
DB 502 VPYLGTFLLDVLMLDTA 518

## RESULT 7

PCT-US95-03552-5  
Sequence 5, Application PC/TUS9503552  
GENERAL INFORMATION:  
APPLICANT: Williams, Lewis T.  
APPLICANT: Demo, Susan  
TITLE OF INVENTION: A Novel ras p21-Interacting Protein and  
TITLE OF INVENTION: Uses Thereof  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03552  
FILING DATE: 20-MAR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 02307K-56800  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 852 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-03552-5

Query Match 2.4%; Score 17; DB 5; Length 852;  
Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 VPYLGTFLLDVLMLDTA 437  
|||||  
DB 502 VPYLGTFLLDVLMLDTA 518

## RESULT 8

Sequence 5, Application PC/TUS9503552  
GENERAL INFORMATION:  
APPLICANT: Williams, Lewis T.  
APPLICANT: Demo, Susan  
TITLE OF INVENTION: A Novel ras p21-Interacting Protein and  
TITLE OF INVENTION: Uses Thereof

US-09-949-016-8733  
Sequence 8733, Application US/09949016  
Patent No. 8812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8733  
LENGTH: 378  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8733

Query Match 1.5%; Score 11; DB 2; Length 378;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 VPYLGTFLLD 431  
|||||  
DB 38 VPYLGTFLLD 48

## RESULT 9

US-10-118-328-5  
Sequence 5, Application US/10118328  
Patent No. 6773904  
GENERAL INFORMATION:  
APPLICANT: YAN, Chunhua et al.  
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,  
NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE  
PROTEINS, AND USES THEREOF  
FILE REFERENCE: CL001220  
CURRENT APPLICATION NUMBER: US/10/118,328  
CURRENT FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/282,460  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 725  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-118-328-5

Query Match 1.5%; Score 11; DB 2; Length 725;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 VPYLGTFLLD 431  
|||||  
DB 409 VPYLGTFLLD 419

## RESULT 10

US-08-408-519-2  
Sequence 2, Application US/08408519  
Patent No. 5955354  
GENERAL INFORMATION:  
APPLICANT: Williams, Lewis T.  
APPLICANT: Demo, Susan  
TITLE OF INVENTION: A No. 5955354el ras p21-Interacting Protein and  
TITLE OF INVENTION: Uses Thereof



```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-03552-2

Query Match 1.5%; Score 11; DB 5; Length 768;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 421 VPYLGTFLTDL 431
Db 417 VPYLGTFLTDL 427

RESULT 12
US-09-270-767-31859
; Sequence 31859, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31859
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-31859

Query Match 1.4%; Score 10; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 422 PYLGTFLTDL 431
Db 50 PYLGTFLTDL 59

RESULT 13
US-09-270-767-47076
; Sequence 47076, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47076
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47076

Query Match 1.4%; Score 10; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 422 PYLGTFLTDL 431
Db 50 PYLGTFLTDL 59

RESULT 14
US-08-820-170A-1

```

; Sequence 1, Application US/08820170A  
; Patent No. 5831058  
; GENERAL INFORMATION:  
; APPLICANT: Tsutomu, FUJIWARA  
; APPLICANT: Takeshi, WATANABE  
; APPLICANT: Masato, HORIE  
; APPLICANT: Toyomasa, KATAGIRI  
; TITLE OF INVENTION: HUMAN GENE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/820,170A  
; FILING DATE:  
; CLASSIFICATION: 536  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 293-7060  
; TELEFAX: (202) 293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-820-170A-1

Query Match 1.3%; Score 9; DB 1; Length 122;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 TSQDKAPSV 643  
Db 16 TSQDKAPSV 24  
|||||

RESULT 15  
US-09-055-699-1  
; Sequence 1, Application US/09055699  
; Patent No. 6005088  
; GENERAL INFORMATION:  
; APPLICANT: Tsutomu, FUJIWARA  
; APPLICANT: Takeshi, WATANABE  
; APPLICANT: Masato, HORIE  
; APPLICANT: Toyomasa, KATAGIRI  
; TITLE OF INVENTION: HUMAN GENE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/055,699  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/820,170  
; FILING DATE:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 293-7060  
; TELEFAX: (202) 293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-055-699-1

Query Match 1.3%; Score 9; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 TSQDKAPSV 643  
Db 16 TSQDKAPSV 24  
|||||

Search completed: June 12, 2006, 12:06:24  
Job time : 54 secs

APPLICANT: Zhao, Qing A.  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Xue, Aidong J.  
APPLICANT: Ren, Feiyan  
APPLICANT: Wang, Dunrui  
APPLICANT: Chen, Rui-hong  
APPLICANT: Drmanac, Radolje T.  
TITLE OF INVENTION: No. US20030096279A1el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 790CIP2D DIVA  
CURRENT APPLICATION NUMBER: US/10/233,131  
CURRENT FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 09/808,701  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: pt\_F1 genes Version 2.0  
SEQ ID NO 33  
LENGTH: 715  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-233-131-33

Query Match 68.6%; Score 487; DB 4; Length 715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 224 DSSEACAEAEGLMPQGLDPSVDEVAEQTLIDLELFSKVLKYECLGSVMSQDRPG 283  
DB 229 DSSEACAEAEGLMPQGLDPSVDEVAEQTLIDLELFSKVLKYECLGSVMSQDRPG 288  
QY 284 AAGASTVTRATVAQFNTVTCVGLSVLGPAGLAAPQRAQLEKWIQAQRCRELNFSSL 343  
DB 289 AAGASTVTRATVAQFNTVTCVGLSVLGPAGLAAPQRAQLEKWIQAQRCRELNFSSL 348  
QY 344 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 403  
DB 349 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 408  
QY 404 EEDNTPGSLSPKPPGPPVPLGTFTDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 463  
DB 409 EEDNTPGSLSPKPPGPPVPLGTFTDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 468  
QY 464 QLQRCQSYTLSPHPPIAALHAQNLTEQSYRLSRVIEPPAASCPSPRIRRRISLTK 523  
DB 469 QLQRCQSYTLSPHPPIAALHAQNLTEQSYRLSRVIEPPAASCPSPRIRRRISLTK 528  
QY 524 RLSAKLAREKSSPSGSGDPSSTSSVSGSPSSPRSRDAPAGSPASPAGPGQGSTKL 583  
DB 529 RLSAKLAREKSSPSGSGDPSSTSSVSGSPSSPRSRDAPAGSPASPAGPGQGSTKL 588  
QY 584 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSV 643  
DB 589 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSV 648  
QY 644 VRRALQKHNVQPWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 703  
DB 649 VRRALQKHNVQPWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 708  
QY 704 TLSVSPS 710  
DB 709 TLSVSPS 715

RESULT 9  
US-10-240-145-85  
; Sequence 85, Application US/10240145  
; Publication No. US2003023588A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 21272-048  
CURRENT APPLICATION NUMBER: US/10/240,145  
CURRENT FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/668,680  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/695,618  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 09/728,711  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: NOT YET ASSIGNED  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: Custom  
SEQ ID NO 85  
LENGTH: 715  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-240-145-85

Query Match 68.6%; Score 487; DB 4; Length 715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 224 DSSEACAEAEGLMPQGLDPSVDEVAEQTLIDLELFSKVLKYECLGSVMSQDRPG 283  
DB 229 DSSEACAEAEGLMPQGLDPSVDEVAEQTLIDLELFSKVLKYECLGSVMSQDRPG 288  
QY 284 AAGASTVTRATVAQFNTVTCVGLSVLGPAGLAAPQRAQLEKWIQAQRCRELNFSSL 343  
DB 289 AAGASTVTRATVAQFNTVTCVGLSVLGPAGLAAPQRAQLEKWIQAQRCRELNFSSL 348  
QY 344 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 403  
DB 349 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 408  
QY 404 EEDNTPGSLSPKPPGPPVPLGTFTDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 463  
DB 409 EEDNTPGSLSPKPPGPPVPLGTFTDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 468  
QY 464 QLQRCQSYTLSPHPPIAALHAQNLTEQSYRLSRVIEPPAASCPSPRIRRRISLTK 523  
DB 469 QLQRCQSYTLSPHPPIAALHAQNLTEQSYRLSRVIEPPAASCPSPRIRRRISLTK 528  
QY 524 RLSAKLAREKSSPSGSGDPSSTSSVSGSPSSPRSRDAPAGSPASPAGPGQGSTKL 583  
DB 529 RLSAKLAREKSSPSGSGDPSSTSSVSGSPSSPRSRDAPAGSPASPAGPGQGSTKL 588  
QY 584 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSV 643  
DB 589 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSV 648  
QY 644 VRRALQKHNVQPWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 703  
DB 649 VRRALQKHNVQPWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 708  
QY 704 TLSVSPS 710  
DB 709 TLSVSPS 715

RESULT 10  
US-10-291-128-85  
; Sequence 85, Application US/10291128  
; Publication No. US2005020242A1  
; GENERAL INFORMATION:  
; APPLICANT: Nuvelo, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP4